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PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

APPLICANT : ROTHSCCHILD, et al.  
SERIAL NO : 09/380,419  
FILED : July 24, 2000  
TITLE : MELANOCORTIN-4 RECEPTOR GENE AND USES AS A  
GENETIC MARKER FOR FAT CONTENT, WEIGHT GAIN,  
AND/OR FEED CONSUMPTION OF ANIMALS

Grp./A.U. : 1655  
Examiner : Einsmann, J.  
Conf. No. : 2593  
Docket No. : P03815US1

AMENDMENT

Assistant Commissioner for Patents  
Washington, D.C. 20231

Sir:

In response to the Office Action dated June 19, 2001, please amend the above-identified application as follows:

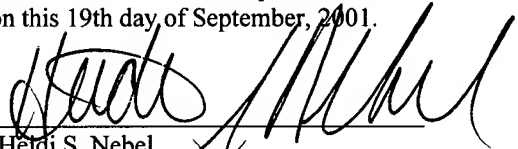
In the Specification

Please replace the paragraph beginning at page 19, line 16, with the following rewritten paragraph:

B1  
PCR amplification of a pig MC4R gene fragment. Primers were designed from homologous regions of human and rat MC4R sequences (GenBank accession no. s77415 and

CERTIFICATE OF MAILING (37 C.F.R. § 1.8(a))

I hereby certify that this document and the documents referred to as enclosed therein are being deposited with the United States Postal Service as First Class mail in an envelope addressed to: Assistant Commissioner for Patents, Washington, D.C. 20231, on this 19th day of September, 2001.

  
Heidi S. Nebel

B1  
cont

u67863, respectively). The primers were: forward primer: 5'-TGG CAA TAG CCA AGA ACA AG-3' (SEQ. ID NO:5) and reverse primer: 5'-CAG GGG ATA GCA ACA GAT GA-3' (SEQ. ID NO:6). The PCR reaction was performed using 12.5 ng of porcine genomic DNA, 1x PCR buffer, 1.5 mM MgCl<sub>2</sub>, 0.125 mM dNTPs, 0.3 mM of each primer, and 0.35 U *Taq* DNA polymerase (Promega) in a 10μL final volume. The conditions for PCR were as follows: 2 min at 94°C; 35 cycles of 30 s at 94°C, 1 min at 56°C, 1 min 30 s at 92°C, and a final 15 min extension at 72°C in a Robocycler (Stratagene, La Jolla, CA).

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In the Claims

Please cancel claims 13-19 and 24-27.

Please amend claims 1, 2, 4-6, 10, 12, 20, 23, 28, 29, 31, 32 as follows:

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1. (Amended)

B2

A method of identifying an animal which possesses a genotype having a genetic marker associated with variation in metabolic traits such as fat content, growth rate, and feed consumption, the method comprising:

- a. obtaining a nucleic acid sample from the animal; and
- b. identifying a genotype characterized by a polymorphism in the seventh transmembrane domain in the MC4R protein wherein, said genotype is associated with variation in metabolic traits such as fat content, growth rate, and feed consumption.

2. (Amended)

The method of claim 1 wherein the polymorphism is characterized by a site specific mutation at amino acid position 298 in the seventh transmembrane domain of the MC4R protein in pigs and any other animal.

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4. (Amended)

The method of claim 2 wherein the polymorphism at amino acid position 298 is associated with variation in fat content.

B3  
5. (Amended)

The method of claim 2 wherein marker for lower feed intake, than animals without marker, is identifiable by a mutation that replaces aspartic acid codon with asparagine codon at amino acid position 298 of MC4R protein.

6. (Amended)

The method of claim 2 wherein marker for faster rate of gain, than animals without marker, is identifiable by a mutation that replaces aspartic acid codon with asparagine codon at amino acid position 298 of the MC4R protein.

B4  
10. (Amended)

The method of claim 1 further comprising the step of amplifying polymorphism in the MC4R gene sequence with allele specific oligonucleotide primers.

B5  
12. (Amended)

The amplified gene sequence of claim 10 wherein primers used in the amplification are selected from the group consisting of SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, and SEQ ID NO: 10.

20. (Amended)

B6  
A method of identifying an animal which possess a desired genotype having a genetic marker associated with metabolic traits such as fat content, growth rate, and feed consumption, the method comprising:

- a) obtaining a nucleic acid sample from an animal;

B6  
cont

- b) amplifying nucleic acid of said sample with primers SEQ ID NO: 5 AND SEQ ID NO: 6.
  - c) digesting the sample with *Taq I* to obtain fragments;
  - d) separating the fragments obtained from the digestion, and
  - e) identifying the presence or absence of a *Taq I* site in an MC4R gene fragment to specify polymorphic site.
- 

B7

23. (Amended)

The method of claim 20 wherein the step of identifying comprises detecting the *Taq I* restriction pattern.

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B8

28. (Amended)

A method for selecting animals for a desired polymorphic traits associated with lower fat content, faster growth rate, or lower feed consumption, than animals without said traits, comprising:

- a) obtaining a nucleic acid sample from an animal;
- b) amplifying the nucleic acid of said sample;
- c) identifying a polymorphism characterized within a *Taq I* restriction recognition site, and
- d) selecting the animals which have a nucleotide substitution of guanine to adenine within the *Taq I* restriction site within the MC4R gene.

29. (Amended)

B8  
cont

A method for an indirect selection for a polymorphism in MC4R wherein specific alleles of an alternative DNA marker are used to make the indirect selection wherein the alternative DNA marker is a linked marker near MC4R comprising utilizing genetic linkage mapping techniques.

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31. (Amended)

A method of identifying animals which possesses a desired genotype having a genetic marker associated with metabolic traits such as fat content, growth rate, and feed consumption to determining the association between a MC4R genotype and a trait of interest, the method comprising:

- B9
- a) obtaining a sample of animals from a line or breed of interest,
  - b) preparing genomic DNA from each animal in the sample,
  - c) determining the genotype of the MC4R gene, and
  - d) calculating the association between the MC4R genotype and the trait.

32. (Amended)

A method of selecting animals which possess a desired MC4R genotype having a genetic marker associated with metabolic traits such as fat content, growth rate, and feed consumption, the method comprising:

- a) obtaining a nucleic acid sample from an animal;
  - b) identifying the genotype of the MC4R gene of the animal; and
  - c) selecting those animals which have the genotype associated with the desired traits.
-

Please add new claim 33.

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33. (New)

B10 A method of identifying an animal which possesses a desired polymorphism within the melanocortin-4 receptor protein of the seventh transmembrane domain comprising:

- a) obtaining a nucleic acid sample from an animal;
  - b) identifying polymorphism by a nucleotide substitution within a *Taq I* site specific restriction pattern of the MC4R gene.
-

## REMARKS

### I. Priority

Applicant acknowledges but refutes Examiners grant of priority. Applicant believes that priority to the screening methods herein extend to the provisional filing date. Since there is no intervening art, applicant will not address this issue. This should not be taken as an acquiescence to the Examiner's position.

### II. Specification

The Examiner has objected to the specification on the basis that it fails to comply with the requirements of the sequencing rules (37 CFR 1.821 –1.825). The application has been amended so that the sequence identifiers in the examples match up with those provided in the sequencing list.

### III. Claim Rejections - 35 U.S.C. § 112, First Paragraph

Claims 1-12, 20-23, and 28-32 stand rejected under 35 U.S.C. 112, first paragraph. The Examiner states that while the specification is enabling for methods of identifying a pig which possesses a genotype indicative of having less back fat and lower feed intake than a pig with a different genotype, it does not reasonably provide enablement for methods which screen other animals or for other methods of utilizing other polymorphisms. The Examiner states that the specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to practice the invention commensurate in scope with these claims. The claims have been amended to more specifically recite the MC4R polymorphism, however, Applicants maintain that one of ordinary skill in the relevant art when reviewing the teachings of Applicant's specification would be able to use the teachings to screen for said polymorphism in other animals.

The Examiner further states that the prior art is silent with respect to other possible polymorphisms in the MC4R gene or with respect to the association of this particular polymorphism with any metabolic trait in any other animal. Applicants have amended claims to more specifically describe the polymorphism associated with variation in metabolic traits within the MC4R protein. In doing so, Applicants have shown that this particular polymorphism is within a highly conserved region among melanocortin receptors (MCR). Moreover, the specification discloses a multiple alignment of the predicted amino acid sequences of the pig MC4R with MC4R proteins from other species showing that the aspartic acid found at position 298 of the seventh transmembrane domain is very highly conserved in the MC4R proteins. Furthermore, Applicants have shown that the MC4R gene consists of approximately 1 kb of coding sequence contained within a single exon with the pig MC4R gene fragment being nearly the entire gene. Additionally, Applicants have shown that the sequence of the PCR product confirms that the PCR product is the MC4R gene with 92.2% and 97.6% identities at the nucleotide and amino acid levels respectively to the human MC4R sequence. By using primers designed from a homologous human and rat MC4R sequences to find this porcine sequence, Applicants demonstrate that the same MC4R gene sequence may be found the same way in other animals.

Further, high identity can be found between the porcine MC4R amino acid sequence and other species. A Blast comparison, attached herewith, of the local alignment of the porcine amino acid sequence showed substantial identity with human at 90%, with mouse at 88%, with cow at 88 %, and with chicken at 81%. Thus, one could easily design primers to assay for this polymorphism in other species.



In addition, the Examiner states the amount of direction or guidance presented in the specification of only one point mutation in the MC4R gene of one species of animal is minimal given the redundancy of the genetic code. “The ‘predictability or lack thereof’ refers to the ability of one skilled in the art to extrapolate the disclosed or known results of the invention. If one skilled in the art can readily anticipate the effect of a change within the subject matter to which the claimed invention pertains, then there is predictability in the art.”

Training Materials For Patent Applications With Respect To 35 U.S.C Section 112, First Paragraph-Enablement Chemical/Biotechnical Applications ( last modified Nov. 5, 1996)

<http://www.uspto.gov/web/offices/pac/dapp/oppd/1pecba.htm>. It is the position of the Applicants that the sequence conservation is such that it is recognizable for those skilled in the art to screen pigs and other animals for this polymorphism. The specification goes into great detail about how to identify the existence of a particular polymorphism in an animal. Once knowledge of the existing polymorphism is known, it would take no more than routine screening to identify the presence of the polymorphism in another species. On page 7 of the specification, the Examiner will please note that a further embodiment of the invention is to provide a breeding method assay done on a plurality of gene sequences from different animals. Such methods after identification of the polymorphism, an embodiment of the invention disclosed on page 6 of the specification, could then be routinely carried out using techniques known to those skilled in the art.

The test for enablement under § 112, first paragraph is “whether or not the specification contains sufficiently explicit disclosure to enable one having ordinary skill in the relevant field to practice the invention claimed therein without the exercise of undue

experimentation.” Ex Parte Forman, 230 U.S.P.Q. 546 (Bd. Pat. App. And Int’f 1986). In this case, the Board stated that:

The test is not merely quantitative, since a considerable amount of experimentation is permissible, if it is merely routine, or if the specification in question provides a reasonable amount of guidance with respect to the direction in which the experimentation should proceed to enable the determination of how to practice the desired embodiment of the invention claimed.

Id. At 547.

Although the specification does not list all the polymorphisms in the MC4R gene, “as long as the specification discloses at least one method for making and using the claimed invention that bears a reasonable correlation to the entire scope of the claim, then the enablement requirement of Section 112 is satisfied.” In re Fisher, 427 F. 2d 833, 839, 166 USPQ 18, 24 (CCPA 1970). Moreover, “failure to disclose other methods by which the claimed invention may be made does not render a claim invalid under Section 112.” Spectra-Physics, Inc. v. Coherent, Inc. 827 F.2d 1524, 1533, 3 USPQ2d 1737, 1743 (Fed. Cir.), cert. denied, 484 U.S. 954 (1987). Additionally claims 1, 28, and 33 are limited to the exact polymorphism.

The Applicants respectfully refute the claim by the Examiner that no evidence in the specification provided that the identified polymorphism is causative of the observed traits. The specification clearly demonstrates that the porcine MC4R missense mutation is significantly associated with several performance traits in pigs. Allele 1 representing the Asp298 was associated with statistically significant decrease in backfat thickness, slower growth rate, and lower feed intake and allele 2, representing Asn 298, was associated with fatter, higher feed intake, and faster growing animals. Thus, there has been a showing of

significant associations of MC4R genotypes with backfat, growth rate, and feed intake.

Whether a polymorphism is a causative mutation is not necessarily conclusive of whether there is a statistical association between the polymorphism and a trait such that it may be useful as a marker for selection.

The Examiner next rejected claims 10 and 24-26 as containing subject matter which was not described in the specification to reasonably convey one of skilled the relevant art that the inventor(s) had possession of the invention at filing. The examiner notes that claim 10 includes an amplification step requiring amplification of the entire MC4R gene and claims 24-26 are drawn to kits comprising a reagent that identifies the polymorphism in an MC4R gene. Furthermore, the Examiner noted that the rejection applied to claims as far as they encompass primers that amplify the MC4R gene from any animal except pig.

Claim 10 has been amended to amplify a polymorphism in the MC4R gene employing a method of allele specific oligonucleotide primers instead of amplification of the entire MC4R gene, to alleviate this rejection.

Claims 24-26 have been cancelled, thereby alleviating this rejection.

#### IV. Claim Rejections-35 U.S.C. § 112, Second Paragraph

Claims 1-23 and 26-32 were rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. Claims 1-23 and 28-32 have been amended to particularly point out and distinctly claim the subject matter as a method of identifying an animal possessing a genotype having a genetic marker based on or within the MC4R gene which is associated with fat content, growth rate, and/or feed consumption, thereby

alleviating this rejection. Claim 26 and 27 have been canceled thereby alleviating this rejection.

Claim 28 has been amended to claim the subject matter of “a method of selecting animals for a desired polymorphic trait associated with lower fat content, faster growth rate, or lower feed.”

Claim 29 has been amended claim the subject matter of “a method for indirect selection for a polymorphism in MC4R using specific alleles of an alternative DNA marker to make the indirect selection using genetic linkage mapping techniques.”

Claim 31 and claim 32 have been amended to claim the subject matter which the applicants regards as their invention, thereby alleviating the rejection. Claim 31 has been amended to claim the subject matter of “a method of identifying animals possessing a desired genotype having a genetic marker associated with metabolic traits such as fat content, growth rate, and feed consumption to determine the association between the MC4R genotype and a trait of interest.” Claim 32 has been amended to claim the subject matter of “a method of identifying animals possessing a desired genotype having a genetic marker associated with metabolic traits such as fat content, growth rate, and feed consumption to select animals expressing the favorable underlying genetic criteria, such as fat content, growth rate, and feed consumption.

The Examiner further states that Claims 1-13, 20-23, and 29-31 are indefinite for failing to recite a final process step which agrees back with the preamble. The Examiner noted that claims 1-13 are drawn to a method for identifying an animal which possesses a genotype indicative of the metabolic traits, yet the claims do not set forth the relationship between identifying the polymorphism and identifying an animal, thereby making it unclear

as to whether the claims are intended to be drawn to a method of identifying an animal or a method of identifying an polymorphism. The claims have been amended to set forth a relationship between the final process step and the preamble to alleviate the rejection.

Claims 1-13, 20-23, and 29-31 have been amended to recite a final processing step with agrees back with the preamble, thereby alleviating the rejection. Claims 1-13 have been amended to provide a method of genetically evaluating animals by assaying for the presence of at least one genetic marker associated with one or more of the traits of fat content, growth rate, and feed consumption.

Claims 20-23 have been amended to provide a method of evaluating animals that increases accuracy in selection and breeding methods for the desired traits.

Claims 29-30 have been amended to indirectly select for the polymorphism with alternative DNA markers and alleles of DNA markers known to be associated with the MC4R gene.

Claims 31 has been amended to provide a method of identifying animals which possess a desired genotype having a genetic marker associated with metabolic traits such as fat content, growth rate, and feed consumption to ascertain the association between a MC4R genotype and a trait of interest.

The Examiner rejected Claims 1-13, 20-23, 31-32 as being indefinite over the recitation “possessing a genotype indicative of the metabolic traits of fat content, growth rate, and feed consumption” because of the uncertainty as to what the genotype is indicating. Claims 1-13, 20-23 and 31-32 have been amended to show that a genotype having the MC4R missense mutation is associated with changes in the metabolic traits such as fat content, growth rate, and feed consumption in pigs and other animals.

Claims 2, 4-6, and 28 were rejected as being indefinite over the recitation of “polymorphism characterized by a nucleotide position” because it does not clearly define the polymorphism. These claims have been amended to characterize the polymorphism “at amino acid position 298 in the seventh transmembrane domain of the MC4R gene in pigs and other animals” thereby alleviating this rejection.

Claims 2, 4-6, 13-19, and 20-23 were rejected because the phrase “the PCR product of the MC4R gene” lacked proper antecedent basis in the claims. Claims 2, 4-6, have been amended by not referring to “the PCR of the MC4R gene”, claims 13-19 have been cancelled, and 20-23 have been amended to add an amplifying step, thereby alleviating this rejection.

The Examiner rejected Claims 2, 4-6, 13-23, and 28 as being indefinite over the recitation “at base 678” or “nucleotide 678” because these claims are referring to a specific nucleotide position of a specific PCR product without including a step which produces the specific PCR product. Claims 2, 4-6 have been amended by claiming a specific polymorphism within the MC4R protein. Claim 28 was further rejected as being indefinite over the recitation of “a PCR product” for the aforementioned reason. Claim 28 has been amended by not referring to a PCR product, rather, identifying the polymorphism as being within a *Taq* I restriction recognition site of the MC4R gene to alleviate the rejection. Claims 13-19 have been cancelled, thereby alleviating the rejection.

Claims 5 and 28 were rejected as being indefinite over the recitation of “lower feed intake” because it is a relative term and the claim does not establish what the feed intake is lower than. Claims 5 and 28 have been amended to show what the term, “lower feed intake” is relative to animals not possessing the polymorphism, thus alleviating the rejection.

Claims 6 and 28 were rejected as being indefinite over the recitation of “faster rate of gain” because it is a relative term and the claims do not establish what the rate of gain is faster than. Claims 6 and 28 have been amended to show that the term “faster rate of gain” is relative to animals not possessing the polymorphism, thereby alleviating the rejection.

Claims 13-19 were rejected over the language “consisting of a nucleotide sequence having” because this is an improper combination of both open and closed claim language. Claims 13-19 have been cancelled, thereby alleviating this rejection.

Claim 26 has been cancelled, thereby alleviating the rejection.

Claim 28 was further rejected as being indefinite because the phrase “the nucleotide associated with the desired traits” lacks proper antecedent basis in the claim. This claim has been amended to avoid indefiniteness by changing claim language.

Claims 29-30 were rejected as being indefinite because they did not contain any method steps which clearly defined the claimed invention. The claims have been amended to have a method step(s) to clearly define the claimed invention.

V. Claimed Rejections – 35 USC § 102

Claim 13 was rejected under 35 USC 102(b) as being anticipated by Studier *et al.* (US 5547843). Claim 13 has been cancelled.

Next, the Examiner rejected Claims 13, 24, 25, and 26 under 35 U.S.C. 102(b) as being anticipated by Boehringer Mannheim 1997 Biochemicals Catalog. Claims 13, 24, 25, and 26 have been cancelled, thereby alleviating this rejection.

Claims 1 and 10 were rejected under 35 U.S.C. 102(a) as being anticipated by Yeo *et al.* These claims were amended by claiming an polymorphism that is characterized as a missense mutation at amino acid position 298 of the seventh transmembrane domain of the

MC4R protein, thereby alleviating this rejection. Further, the polymorphism has been characterized at the nucleotide level as a site-specific mutation occurring within a *Taq I* restriction enzyme recognition site. Conversely, Yeo teaches a method of identifying a human which possesses a genotype indicative of the metabolic trait of fat content comprising obtaining a nucleic acid sample from the subject and identifying a polymorphism in the MC4R gene of the sample, which involves amplifying the MC4R gene. Moreover, Yeo discloses a method of identifying a frameshift mutation in MC4R, which disrupts the fifth transmembrane domain. The Federal Circuit in W.L. Gore & Associates v. Garlock, Inc., stated that “[a]nticipation requires the disclosure in a single prior art reference of each element of the claim under consideration. W.L. Gore & Associates v. Garlock, Inc. 721 F2d. 1540, 220 USPQ 303, 313, *cert. denied*, 469 U.S. 851 (1984) (citing Sounscriber Corp. v. United States, 360 F2d 954, 960, 148 USPQ 298, 301 (Ct. Cl., adopted, 149 USPQ 640 (Ct. Cl. 1966)). Yeo fails to teach a method of identifying a missense mutation at amino acid position 298 of the seventh transmembrane domain in the MC4R protein, therefore, Applicants’ claim is not anticipated. Applicants respectfully request reconsideration and withdrawal of the objection under 35 U.S.C. 102(a).

VI. Claims Rejections – 35 USC § 103

Claims 13, 14, 16 and 18 were rejected under 35 U.S.C 103(a) as being unpatentable over Yamada *et al.* (US 5703220) in view of Hogan *et al.* (US 5595874). Claims 14, 15, 18, and 19 have been cancelled, thus alleviating the rejection.

Claims 24-27 were rejected under 35 U.S.C. 103(a) as being unpatentable over Yamada in view of Hogan as applied to claims 13, 14, 16, and 18 and in further view of the



Stratagene Catalog (1998). Claims 24-27 have been cancelled, there by alleviating the rejection.

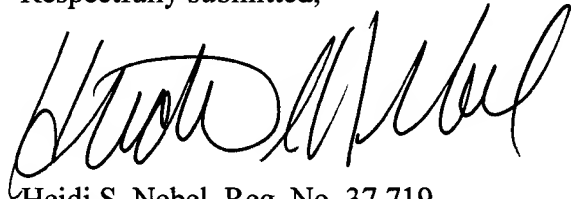
VII. Conclusion

For the above stated reasons, it is believed that application is in a prima facie condition for allowance. Allowance is respectfully requested.

No fees or extensions of time are believed to be due in connection with this amendment; however, consider this a request for any extension inadvertently omitted, and charge any additional fees to Deposit Account No. 26-0084.

Attached hereto is a marked-up version of the changes made to the specification and claims by the current amendment. The attached page is captioned "Version with marking to show changes made."

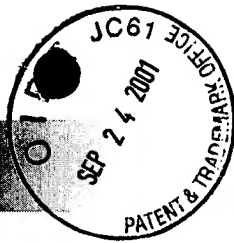
Respectfully submitted,



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Attorneys of Record

- pw -



# results of BLAST

BLASTP 2.2.1 [Apr-13-2001]

**Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1000769210-15253-3406

**Query=**

(332 letters)

**Database: nr**

760,566 sequences; 242,018,981 total letters

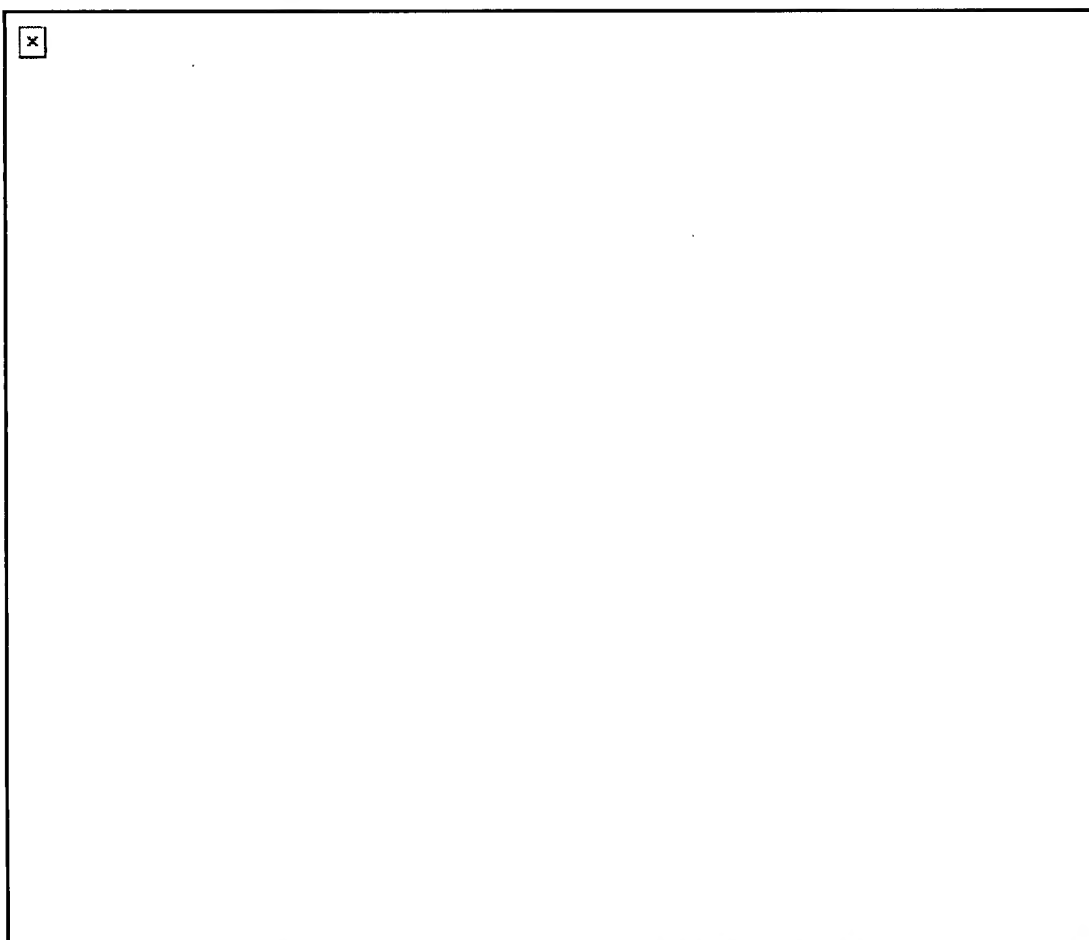
If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

## Distribution of 582 Blast Hits on the Query Sequence

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Mouse-over to show define and scores. Click to show alignments



Sequences producing significant alignments:			Score	E
			(bits)	Value
gi 10720085 sp O97504 MC4R_PIG	MELANOCORTIN-4 RECEPTOR (MC4...	556	e-158	
gi 11424669 ref XP_008716.1	melanocortin 4 receptor [Homo ...	531	e-150	
gi 5174533 ref NP_005903.1	melanocortin 4 receptor [Homo s...	530	e-150	
gi 2494982 sp P70596 MC4R_RAT	MELANOCORTIN-4 RECEPTOR (MC4...	529	e-149	
gi 1362861 pir A57055	melanocortin receptor 4 - human >gi ...	529	e-149	
gi 11493679 qb AAG35602.1 AF201662_1	(AF201662) melanocorti...	528	e-149	
gi 13629481 sp Q9GLJ8 MC4R_BOVIN	MELANOCORTIN-4 RECEPTOR (M...	519	e-146	
gi 2981626 dbj BAA25252.1	(AB012211) melanocortin 4-recept...	488	e-137	
gi 6940719 qb AAF31753.1	(AF087937) melanocortin-4 recepto...	389	e-107	
gi 3061273 dbj BAA25640.1	(AB012868) melanocortin 5-recept...	339	2e-92	
gi 7305263 ref NP_038624.1	melanocortin 5 receptor [Mus mu...	333	1e-90	
gi 13629514 sp Q9TT23 MC5R_PANTR	MELANOCORTIN-5 RECEPTOR (M...	325	2e-88	
gi 5174535 ref NP_005904.1	melanocortin 5 receptor [Homo s...	325	3e-88	
gi 7447148 pir JC5592	melanocortin 5 receptor - human >gi ...	324	8e-88	
gi 6981190 ref NP_037314.1	melanocortin 5 receptor [Rattus...	322	3e-87	
gi 729997 sp P41149 MC5R_MOUSE	MELANOCORTIN-5 RECEPTOR (MC5...	320	1e-86	
gi 468378 qb AAA21337.1	(L22527) melanocortin-5 receptor [...	318	3e-86	
gi 627524 pir JN0764	melanocortin receptor 2 - human	318	3e-86	
gi 1363304 pir B57055	melanocortin-4 receptor - rat (fragm...	317	1e-85	
gi 422989 pir B46647	melanocortin receptor 3 - human >gi 2...	309	2e-83	
gi 6678822 ref NP_032587.1	melanocortin 3 receptor [Mus mu...	307	7e-83	
gi 3493361 dbj BAA32555.1	(AB017137) melanocortin 3-recept...	307	7e-83	
gi 9845271 ref NP_063941.1	melanocortin 3 receptor [Homo s...	306	2e-82	

gi 11420991 ref XP_009545.1	melanocortin 3 receptor [Homo ...	306	2e-82
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gi 1170884 sp P41983 MC5R_SHEEP	MELANOCORTIN-5 RECEPTOR (MC...	300	1e-80
gi 417279 sp P32244 MC3R_RAT	MELANOCORTIN-3 RECEPTOR (MC3-R...	297	8e-80
gi 13629395 sp Q9MZV8 MC5R_PIG	MELANOCORTIN-5 RECEPTOR >gi ...	293	2e-78
gi 3024117 sp P56450 MC4R_MOUSE	MELANOCORTIN-4 RECEPTOR (MC...	271	7e-72
gi 7447146 pir S71420	melanocortin 1 receptor - chicken	256	2e-67
gi 13958120 qb AAK50813.1	(AF362606) melanocortin 1 recept...	253	1e-66
gi 13958058 qb AAK50782.1	(AF362575) melanocortin 1 recept...	253	2e-66
gi 13958064 qb AAK50785.1	(AF362578) melanocortin 1 recept...	252	3e-66
gi 13958076 qb AAK50791.1	(AF362584) melanocortin 1 recept...	252	3e-66
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gi 13958112 qb AAK50809.1	(AF362602) melanocortin 1 recept...	249	2e-65
gi 2134364 pir S70005	melanocortin 1 receptor - chicken	249	2e-65
gi 6091553 qb AAC48590.2	(U39469) alpha melanocyte stimula...	249	3e-65
gi 631554 pir S45708	MSH receptor - bovine >gi 547326 gb A...	248	4e-65
gi 2851404 sp P47798 MSHR_BOVIN	MELANOCYTE STIMULATING HORM...	248	4e-65
gi 3024181 sp P56447 MSHR_OVIMO	MELANOCYTE STIMULATING HORM...	244	7e-64
gi 3024178 sp P56444 MSHR_CAPHI	MELANOCYTE STIMULATING HORM...	243	1e-63
gi 3024173 sp O19037 MSHR_SHEEP	MELANOCYTE STIMULATING HORM...	243	2e-63
gi 3024177 sp P56443 MSHR_CAPCA	MELANOCYTE STIMULATING HORM...	242	4e-63
gi 14599450 qb AAK70924.1 AF288357_1	(AF288357) melanocorti...	241	5e-63
gi 14276855 qb AAK58422.1 AF326520_1	(AF326520) melanocorti...	241	7e-63
gi 3024176 sp P56442 MSHR_ALCAA	MELANOCYTE STIMULATING HORM...	241	9e-63
gi 2696658 dbj BAA24002.1	(AB009605) melanocortin 2-recept...	240	2e-62
gi 3024179 sp P56445 MSHR_CEREL	MELANOCYTE STIMULATING HORM...	239	4e-62
gi 3024182 sp P56448 MSHR_RANTA	MELANOCYTE STIMULATING HORM...	238	5e-62
gi 5257480 qb AAD41355.1 AF153437_1	(AF153437) melanocortin...	238	8e-62
gi 14776691 ref XP_008010.2	melanocortin 1 receptor (alpha...	237	8e-62
gi 5729916 ref NP_002377.2	melanocortin 1 receptor (alpha ...	237	8e-62
gi 3024180 sp P56446 MSHR_DAMDA	MELANOCYTE STIMULATING HORM...	237	8e-62
gi 5834414 qb AAD53963.1 AF181964_1	(AF181964) melanocortin...	237	1e-61
gi 5257478 qb AAD41353.1 AF153435_1	(AF153435) melanocortin...	237	1e-61
gi 14279199 qb AAK58525.1 AF263461_1	(AF263461) melanocorti...	237	1e-61
gi 13631306 sp Q9TUK4 MSHR_PANTR	MELANOCYTE STIMULATING HOR...	236	1e-61
gi 7447147 pir S29204	melanotropin receptor - human	236	2e-61
gi 34791 emb CAA46588.1	(X65634) melanocyte stimulating h...	236	2e-61
gi 6678818 ref NP_032585.1	melanocortin 1 receptor [Mus mu...	236	2e-61
gi 14043809 qb AAH07856.1 AAH07856	(BC007856) Unknown (prot...	236	2e-61
gi 5257475 qb AAD41350.1 AF153432_1	(AF153432) melanocortin...	236	2e-61
gi 5257476 qb AAD41351.1 AF153433_1	(AF153433) melanocortin...	235	5e-61
gi 3024183 sp P79166 MSHR_HORSE	MELANOCYTE STIMULATING HORM...	232	4e-60
gi 299418 qb AAB26087.1	alpha-melanocyte-stimulating hormo...	231	6e-60
gi 13629953 sp Q9TU05 MSHR_PIG	MELANOCYTE STIMULATING HORMO...	230	1e-59
gi 3123250 sp Q29154 MSHR_VULVU	MELANOCYTE STIMULATING HORM...	228	5e-59
gi 4505127 ref NP_000520.1	melanocortin 2 receptor; Melano...	228	6e-59
gi 10720095 sp O77616 MSHR_CANFA	MELANOCYTE STIMULATING HOR...	228	6e-59
gi 2494981 sp P70115 ACTR_MESAU	ADRENOCORTICOTROPIC HORMONE...	227	9e-59
gi 299420 qb AAB26089.1	adrenocorticotropic hormone recept...	227	1e-58
gi 631540 pir S42767	adrenocorticotropic hormone receptor ...	227	1e-58
gi 6678820 ref NP_032586.1	melanocortin 2 receptor; adreno...	226	2e-58
gi 461464 sp P34974 ACTR_BOVIN	ADRENOCORTICOTROPIC HORMONE ...	226	3e-58
gi 1083202 pir JC4046	adrenocorticotropin receptor - mouse	225	3e-58
gi 13626093 sp Q9TU77 ACTR_SHEEP	ADRENOCORTICOTROPIC HORMON...	225	5e-58
gi 2136755 pir I45849	gene ACTH receptor protein - bovine ...	220	1e-56
gi 10719872 sp Q9Z1S9 ACTR_CAVPO	ADRENOCORTICOTROPIC HORMON...	211	9e-54
gi 4262331 qb AAD14570.1	(AF082488) melanocortin receptor ...	201	6e-51

gi 4262329 qb AAD14569.1	(AF082487) melanocortin receptor ...	200	2e-50
gi 4262335 qb AAD14572.1	(AF082490) melanocortin receptor ...	199	2e-50
gi 4262333 qb AAD14571.1	(AF082489) melanocortin receptor ...	198	7e-50
gi 4929144 qb AAD33876.1 AF141365_1	(AF141365) melanocyte s...	174	1e-42
gi 3790627 qb AAC68702.1	(AF097749) melanocyte stimulating...	174	1e-42
gi 4929142 qb AAD33875.1 AF141364_1	(AF141364) melanocyte s...	174	1e-42
gi 4929140 qb AAD33874.1 AF141363_1	(AF141363) melanocyte s...	173	2e-42
gi 2724060 qb AAB96911.1	(AF039388) melanocyte-stimulating...	153	2e-36
gi 9581875 qb AAF89104.1 AF252541_1	(AF252541) melanocyte-s...	151	6e-36
gi 3139154 qb AAC16735.1	(AF064077) adrenocorticotrophic ho...	145	4e-34
gi 8393290 ref NP_058997.1	endothelial differentiation sph...	92	5e-18
gi 12835864 dbj BAB23393.1	(AK004591) putative [Mus musculus]	92	8e-18
gi 119130 sp P21453 EDG1_HUMAN	PROBABLE G PROTEIN-COUPLED R...	92	9e-18
gi 11422839 ref XP_001499.1	endothelial differentiation, s...	91	2e-17
gi 12829875 qb AAK01973.1	(AY011704) EDG1 [Muscardinus ave...	91	2e-17
gi 2495029 sp O08530 EDG1_MOUSE	PROBABLE G PROTEIN-COUPLED ...	91	2e-17
gi 12829879 qb AAK01975.1	(AY011706) EDG1 [Mus musculus]	91	2e-17

## Alignments

>gi|10720085|sp|O97504|MC4R\_PIG MELANOCORTIN-4 RECEPTOR (MC4-R)  
 gi|4062865|dbj|BAA36170.1| (AB021664) melanocortin 4 receptor [Sus scrofa]  
 Length = 332

Score = 556 bits (1434), Expect = e-158  
 Identities = 313/332 (94%), Positives = 313/332 (94%)

Query: 1 MNSTHHHGMHTSLHFWNRSTYGLHSNASEPLGKGYSEGGCYEQLFVSPEVFTLGVISLL 60  
 MNSTHHHGMHTSLHFWNRSTYGLHSNASEPLGKGYSEGGCYEQLFVSPEVFTLGVISLL  
 Sbjct: 1 MNSTHHHGMHTSLHFWNRSTYGLHSNASEPLGKGYSEGGCYEQLFVSPEVFTLGVISLL 60

Query: 61 ENILVIVAI AKNKNLHSPMYFFICSLAVADMLVSVSNGSETIVITLLNSTDTDAQSFTVN 120  
 ENILVIVAI AKNKNLHSPMYFFICSLAVADMLVSVSNGSETIVITLLNSTDTDAQSFTVN  
 Sbjct: 61 ENILVIVAI AKNKNLHSPMYFFICSLAVADMLVSVSNGSETIVITLLNSTDTDAQSFTVN 120

Query: 121 IDNVIDXXXXXXXXXXXXXXXXXXXXDRYFTIFYALQYHNIMTVKRVGIIISCIWAVCTVS 180  
 IDNVID DRYFTIFYALQYHNIMTVKRVGIIISCIWAVCTVS  
 Sbjct: 121 IDNVIDSVICSSLLASICSLLSIAVDYFTIFYALQYHNIMTVKRVGIIISCIWAVCTVS 180

Query: 181 GVLFIISDSSAVIICLITVFFTMLALMASLYVHMFLMARLHIKRIAVLPGTGTIRQGAN 240  
 GVLFIISDSSAVIICLITVFFTMLALMASLYVHMFLMARLHIKRIAVLPGTGTIRQGAN  
 Sbjct: 181 GVLFIISDSSAVIICLITVFFTMLALMASLYVHMFLMARLHIKRIAVLPGTGTIRQGAN 240

Query: 241 MKGAILTLILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300  
 MKGAILTLILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL  
 Sbjct: 241 MKGAILTLILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300

Query: 301 IYALRSQELRKTFKEIICCYPLGGLCDLSSRY 332  
 IYALRSQELRKTFKEIICCYPLGGLCDLSSRY  
 Sbjct: 301 IYALRSQELRKTFKEIICCYPLGGLCDLSSRY 332

>gi|11424669|ref|XP\_008716.1| melanocortin 4 receptor [Homo sapiens]  
 Length = 332

Score = 531 bits (1369), Expect = e-150  
 Identities = 301/332 (90%), Positives = 306/332 (91%), Gaps = 1/332 (0%)

Query: 1 MNSTHHHGMHTSLHFWNRSTYGLHSNASEPLGKGYSEGGCYEQLFVSPEVFTLGVISLL 60

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+NST H GMHTSLH WNRS+Y LHSNASE LGKGYS+GGCYEQLFVSPEVFVTLGVISLL
Sbjct: 2 VNST-HRGMHTSLHLWNRSSYRLHSNASESLGKGYS DGGCYEQLFVSPEVFVTLGVISLL 60

Query: 61 ENILVIVAI AKNKNLHSPMYFFICSLAVADMLVSVSNGSETIVITLLNSTDTDAQSFTVN 120
          ENILVIVAI AKNKNLHSPMYFFICSLAVADMLVSVSNGSETIVITLLNSTDTDAQSFTVN
Sbjct: 61 ENILVIVAI AKNKNLHSPMYFFICSLAVADMLVSVSNGSETIVITLLNSTDTDAQSFTVN 120

Query: 121 IDNVIDXXXXXXXXXXXXXXXXXXXXRYFTIFYALQYHNIMTVKRVGIIISCIWAVCTVS 180
          IDNVID DRYFTIFYALQYHNIMTVKRVGIIISCIWA CTVS
Sbjct: 121 IDNVIDSVICSSLLASICSLLSIAVDRYFTIFYALQYHNIMTVKRVGIIISCIWA ACTVS 180

Query: 181 GVLFIISDSSAVIICLITVFFTMLALMASLYVHMFLMARLHIKRIAVLPGTG TIRQGAN 240
          G+LFIISDSSAVIICLIT+FFTMLALMASLYVHMFLMARLHIKRIAVLPGTG IRQGAN
Sbjct: 181 GILFIISDSSAVIICLITMFFTMLALMASLYVHMFLMARLHIKRIAVLPGTG AIRQGAN 240

Query: 241 MKGAITLTILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFM SHFNLYLILIMCNSIIDPL 300
          MKGAITLTILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFM SHFNLYLILIMCNSIIDPL
Sbjct: 241 MKGAITLTILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFM SHFNLYLILIMCNSIIDPL 300

Query: 301 IYALRSQELRKTFKEIICCYPLGGLCDLSSRY 332
          IYALRSQELRKTFKEIICCYPLGGLCDLSSRY
Sbjct: 301 IYALRSQELRKTFKEIICCYPLGGLCDLSSRY 332

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>gi|5174533|ref|NP_005903.1| melanocortin 4 receptor [Homo sapiens]
gi|417280|sp|P32245|MC4R_HUMAN MELANOCORTIN-4 RECEPTOR (MC4-R)
gi|291978|gb|AAA35791.1| (L08603) melanocortin 4 receptor [Homo sapiens]
Length = 332

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Score = 530 bits (1366), Expect = e-150
Identities = 300/332 (90%), Positives = 306/332 (91%), Gaps = 1/332 (0%)

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Query: 1 MNSTHHHGMHTSLHFWNRSTYGLHSNASEPLGKGYS EGGCYEQLFVSPEVFVTLGVISLL 60
          +NST H GMHTSLH WNRS+Y LHSNASE LGKGYS+GGCYEQLFVSPEVFVTLGVISLL
Sbjct: 2 VNST-HRGMHTSLHLWNRSSYRLHSNASESLGKGYS DGGCYEQLFVSPEVFVTLGVISLL 60

Query: 61 ENILVIVAI AKNKNLHSPMYFFICSLAVADMLVSVSNGSETIVITLLNSTDTDAQSFTVN 120
          ENILVIVAI AKNKNLHSPMYFFICSLAVADMLVSVSNGSETI+ITLLNSTDTDAQSFTVN
Sbjct: 61 ENILVIVAI AKNKNLHSPMYFFICSLAVADMLVSVSNGSETIIITLLNSTDTDAQSFTVN 120

Query: 121 IDNVIDXXXXXXXXXXXXXXXXXXXXRYFTIFYALQYHNIMTVKRVGIIISCIWAVCTVS 180
          IDNVID DRYFTIFYALQYHNIMTVKRVGIIISCIWA CTVS
Sbjct: 121 IDNVIDSVICSSLLASICSLLSIAVDRYFTIFYALQYHNIMTVKRVGIIISCIWA ACTVS 180

Query: 181 GVLFIISDSSAVIICLITVFFTMLALMASLYVHMFLMARLHIKRIAVLPGTG TIRQGAN 240
          G+LFIISDSSAVIICLIT+FFTMLALMASLYVHMFLMARLHIKRIAVLPGTG IRQGAN
Sbjct: 181 GILFIISDSSAVIICLITMFFTMLALMASLYVHMFLMARLHIKRIAVLPGTG AIRQGAN 240

Query: 241 MKGAITLTILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFM SHFNLYLILIMCNSIIDPL 300
          MKGAITLTILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFM SHFNLYLILIMCNSIIDPL
Sbjct: 241 MKGAITLTILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFM SHFNLYLILIMCNSIIDPL 300

Query: 301 IYALRSQELRKTFKEIICCYPLGGLCDLSSRY 332
          IYALRSQELRKTFKEIICCYPLGGLCDLSSRY
Sbjct: 301 IYALRSQELRKTFKEIICCYPLGGLCDLSSRY 332

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>gi|2494982|sp|P70596|MC4R_RAT MELANOCORTIN-4 RECEPTOR (MC4-R)

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gi|1565665|qb|AAB36517.1| (U67863) melanocortin-4 receptor [Rattus norvegicus]  
Length = 332

Score = 529 bits (1363), Expect = e-149  
Identities = 293/332 (88%), Positives = 305/332 (91%)

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Query: 1  MNSTHHHGMHTSLHFWNRSTYGLHSNASEPLGKGYSSEGGCYEQLFVSPEVFTLVGLVISLL 60
          MNSTHHHGM+TSLH WNRS++GLH NASE LGKG+S+GGCYEQLFVSPEVFTLVGLVISLL
Sbjct: 1  MNSTHHHGMYSLSHLWNRSSHLHGNASESLGKGHSDGGCYEQLFVSPEVFTLVGLVISLL 60

Query: 61  ENILVIVAIKKNLHSPMYFFICSLAVADMLVSVSNGSETIVITLLNSTDTDAQSFTVN 120
          ENILVIVAIKKNLHSPMYFFICSLAVADMLVSVSNGSETIVITLLNSTDTDAQSFTVN
Sbjct: 61  ENILVIVAIKKNLHSPMYFFICSLAVADMLVSVSNGSETIVITLLNSTDTDAQSFTVN 120

Query: 121 IDNVIDXXXXXXXXXXXXXXXXXXXXXDRYFTIFYALQYHNIMTVKRVGIIISCIWAVCTVS 180
          IDNVID                      DRYFTIFYALQYHNIMTV+RVGIIISCIWA CTVS
Sbjct: 121 IDNVIDSVICSSLLASICSLLSIAVDYFTIFYALQYHNIMTVRRVGIIISCIWAACCTVS 180

Query: 181 GVLFIISDSSAVIICLITVFFTMLALMASLYVHMFLMARLHIKRIAVLPGTGTIRQGAN 240
          GVLFIISDSSAVIICLIT+FFTML LMASLYVHMFLMARLHIKRIAVLPGTGTIRQGAN
Sbjct: 181 GVLFIISDSSAVIICLITMFFTMLVLMASLYVHMFLMARLHIKRIAVLPGTGTIRQGAN 240

Query: 241 MKGAILTLTILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
          MKGAILTLTILIGVFVVCWAPFFLHL+FYISCPQNPYCVCFMSHFNLYLILIMCN++IDPL
Sbjct: 241 MKGAILTLTILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNAVIDPL 300

Query: 301 IYALRSQELRKTFKEIICCYPLGGLCDLSSRY 332
          IYALRSQELRKTFKEIIC YPLGG+C+L RY
Sbjct: 301 IYALRSQELRKTFKEIICFYPLGGICELPGRY 332
```

>gi|1362861|pir|A57055 melanocortin receptor 4 - human  
gi|998457|qb|AAB33341.1| (S77415) melanocortin-4 receptor; hMC4-R [Homo sapiens]  
Length = 332

Score = 529 bits (1362), Expect = e-149  
Identities = 299/332 (90%), Positives = 305/332 (91%), Gaps = 1/332 (0%)

```
Query: 1  MNSTHHHGMHTSLHFWNRSTYGLHSNASEPLGKGYSSEGGCYEQLFVSPEVFTLVGLVISLL 60
          +NST H GMHTSLH WNRS+Y LHSNASE LGKGYS+GGCYEQLFVSPEVFTLVGLVISLL
Sbjct: 2  VNST-HRGMHTSLHLWNRSSYRLHSNASESLGKGYSDDGGCYEQLFVSPEVFTLVGLVISLL 60

Query: 61  ENILVIVAIKKNLHSPMYFFICSLAVADMLVSVSNGSETIVITLLNSTDTDAQSFTVN 120
          ENILVIVAIKKNLHSPMYFFICSLAVADMLVSVSNGSETI+ITLLNSTDTDAQSFTVN
Sbjct: 61  ENILVIVAIKKNLHSPMYFFICSLAVADMLVSVSNGSETIIITLLNSTDTDAQSFTVN 120

Query: 121 IDNVIDXXXXXXXXXXXXXXXXXXXXXDRYFTIFYALQYHNIMTVKRVGIIISCIWAVCTVS 180
          IDNVID                      DRYFTIFYALQYHNIMTVKRVGI ISCIWA CTVS
Sbjct: 121 IDNVIDSVICSSLLASICSLLSIAVDYFTIFYALQYHNIMTVKRVGISISCIWAACCTVS 180

Query: 181 GVLFIISDSSAVIICLITVFFTMLALMASLYVHMFLMARLHIKRIAVLPGTGTIRQGAN 240
          G+LFIISDSSAVIICLIT+FFTMLALMASLYVHMFLMARLHIKRIAVLPGTG IRQGAN
Sbjct: 181 GILFIISDSSAVIICLITMFFTMLALMASLYVHMFLMARLHIKRIAVLPGTGAIHQGAN 240

Query: 241 MKGAILTLTILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
          MKGAILTLTILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL
Sbjct: 241 MKGAILTLTILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300

Query: 301 IYALRSQELRKTFKEIICCYPLGGLCDLSSRY 332
```

IYALRSQELRKTFKEIICCYPLGGLCDLSSRY  
 Sbjct: 301 IYALRSQELRKTFKEIICCYPLGGLCDLSSRY 332

>gi|11493679|qb|AAG35602.1|AF201662\_1 (AF201662) melanocortin-4 receptor [Mus muscul  
 Length = 332

Score = 528 bits (1361), Expect = e-149  
 Identities = 294/332 (88%), Positives = 306/332 (91%)

Query: 1 MNSTHHHGMHTSLHFWNRSTYGLHSNASEPLGKGYSEGGCYEQLFVSPEVFVTLGVISLL 60  
 MNSTHHHGM+TSLH WNRS+YGLHSNASE LGKG+ +GGCYEQLFVSPEVFVTLGVISLL  
 Sbjct: 1 MNSTHHHGMYSLHLWNRSSYGLHSNASESLGKGHPDGGCYEQLFVSPEVFVTLGVISLL 60

Query: 61 ENILVIVAIKKNLHSPMYFFICSLAVADMLVSVSNGSETIVITLLNSTDTDAQSFTVN 120  
 ENILVIVAIKKNLHSPMYFFICSLAVADMLVSVSNGSETIVITLLNSTDTDAQSFTVN  
 Sbjct: 61 ENILVIVAIKKNLHSPMYFFICSLAVADMLVSVSNGSETIVITLLNSTDTDAQSFTVN 120

Query: 121 IDNVIDXXXXXXXXXXXXXXXXXXXXXDRYFTIFYALQYHNIMTVKRVGIIISCIWAVCTVS 180  
 IDNVID DRYFTIFYALQYHNIMTV+RVGIIISCIWA CTVS  
 Sbjct: 121 IDNVIDSVICSSLLASICSLLSIAVDYFTIFYALQYHNIMTVRRVGIIISCIWAACCTVS 180

Query: 181 GVLFIISDSSAVIICLITVFFTMLALMASLYVHMFLMARLHIKRIAVLPGTGTIRQGAN 240  
 GVLFIISDSSAVIICLI++FFTML LMASLYVHMFLMARLHIKRIAVLPGTGTIRQG N  
 Sbjct: 181 GVLFIISDSSAVIICLISMFFTMLVLMASLYVHMFLMARLHIKRIAVLPGTGTIRQGTN 240

Query: 241 MKGAITLTILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300  
 MKGAITLTILIGVFVVCWAPFFLHL+FYISCPQNPYCVCFMSHFNLYLILIMCN++IDPL  
 Sbjct: 241 MKGAITLTILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNAVIDPL 300

Query: 301 IYALRSQELRKTFKEIICCYPLGGLCDLSSRY 332  
 IYALRSQELRKTFKEIIC YPLGG+C+LSSRY  
 Sbjct: 301 IYALRSQELRKTFKEIICFYPLGGICELSSRY 332

>gi|13629481|sp|Q9GLJ8|MC4R\_BOVIN MELANOCORTIN-4 RECEPTOR (MC4-R)  
 gi|10443911|qb|AAG17639.1|AF265221\_1 (AF265221) melanocortin 4 receptor [Bos taurus  
 Length = 332

Score = 519 bits (1336), Expect = e-146  
 Identities = 293/332 (88%), Positives = 299/332 (89%)

Query: 1 MNSTHHHGMHTSLHFWNRSTYGLHSNASEPLGKGYSEGGCYEQLFVSPEVFVTLGVISLL 60  
 MNST GMHTSLH WNRS +G+ +N SE L KGYS+GGCYEQLFVSPEVFVTLGVISLL  
 Sbjct: 1 MNSTQPLGMHTSLHSWNRSAGMPTNVSESLAKGYSDGGCYEQLFVSPEVFVTLGVISLL 60

Query: 61 ENILVIVAIKKNLHSPMYFFICSLAVADMLVSVSNGSETIVITLLNSTDTDAQSFTVN 120  
 ENILVIVAIKKNLHSPMYFFICSLAVADMLVSVSNGSETIVITLLNSTDTDAQSFTV+  
 Sbjct: 61 ENILVIVAIKKNLHSPMYFFICSLAVADMLVSVSNGSETIVITLLNSTDTDAQSFTVD 120

Query: 121 IDNVIDXXXXXXXXXXXXXXXXXXXXXDRYFTIFYALQYHNIMTVKRVGIIISCIWAVCTVS 180  
 IDNVID DRYFTIFYALQYHNIMTVKRV I IS IWA CTVS  
 Sbjct: 121 IDNVIDSVICSSLLASICSLLSIAVDYFTIFYALQYHNIMTVKRVAITISAIWAACCTVS 180

Query: 181 GVLFIISDSSAVIICLITVFFTMLALMASLYVHMFLMARLHIKRIAVLPGTGTIRQGAN 240  
 GVLFIISDSSAVIICLITVFFTMLALMASLYVHMFLMARLHIKRIAVLPG+GTIRQGAN  
 Sbjct: 181 GVLFIISDSSAVIICLITVFFTMLALMASLYVHMFLMARLHIKRIAVLPGSGTIRQGAN 240



Query: 241 MKGAITLTILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300  
 MKGAITLTILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL  
 Sbjct: 241 MKGAITLTILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300

Query: 301 IYALRSQELRKTFKEIICCYPLGGLCDLSSRY 332  
 IYALRSQELRKTFKEIICC PLGGLCDLSSRY  
 Sbjct: 301 IYALRSQELRKTFKEIICCSPLGGLCDLSSRY 332

>gi|2981626|dbj|BAA25252.1| (AB012211) melanocortin 4-receptor [Gallus gallus]  
 Length = 331

Score = 488 bits (1257), Expect = e-137  
 Identities = 272/332 (81%), Positives = 287/332 (85%), Gaps = 1/332 (0%)

Query: 1 MNSTHHHGMHTSLHFWNRSTYGLHSNASEPLGKGYSEGGCYEQLFVSPEVFVTLGVISLL 60  
 MN T H G LHFVN+S GLH ASEP KG+S GGCYEQLFVSPEVFVTLG+ISLL  
 Sbjct: 1 MNFTQHRGTLQPLHFWNQSN-GLHRGASEPSAKGHSSGGCYEQLFVSPEVFVTLGIISLL 59

Query: 61 ENILVIVAIKKNLHSPMYFFICSLAVADMLVSVSNGSETIVITLLNSTDTDAQSFTVN 120  
 EN+LVIVAIKKNLHSPMYFFICSLAVADMLVSVSNGSETIVITLLN+TDTDAQSFT+N  
 Sbjct: 60 ENVLVIVAIKKNLHSPMYFFICSLAVADMLVSVSNGSETIVITLLNNTDTDAQSFTIN 119

Query: 121 IDNVIDXXXXXXXXXXXXXXXXXXXXRYFTIFYALQYHNIMTVKRVGIIISCIWAVCTVS 180  
 IDNVID DRYFTIFYALQYHNIMTVKRVG+II+CIWA CTVS  
 Sbjct: 120 IDNVIDSVICSSLLASICSLLSIAVDYFTIFYALQYHNIMTVKRVGVIITCIWAACCTVS 179

Query: 181 GVLFIISDSSAVIICLITVFFTMLALMASLYVHMFLMARLHIKRIAVLPGTG TIRQGAN 240  
 G+LFIISDSS VIICLI++FFTML LMASLYVHMF+MAR+HIK+IAVLPGTG IRQGAN  
 Sbjct: 180 GILFIISDSSVVIICLISMFFTMLILMASLYVHMFMARMHIKKIAVLPGTGPIRQGAN 239

Query: 241 MKGAITLTILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300  
 MKGAITLTILIGVFVVCWAPFFLHLIFYISCP NPYCVCFMSHFN YLILIMCNSIIDPL  
 Sbjct: 240 MKGAITLTILIGVFVVCWAPFFLHLIFYISCPNPNPYCVCFMSHFNLYLILIMCNSIIDPL 299

Query: 301 IYALRSQELRKTFKEIICCYPLGGLCDLSSRY 332  
 IYA RSQELRKTFKEIICC L GLCDL +Y  
 Sbjct: 300 IYAFRSQELRKTFKEIICCNLRGLCDLPGKY 331

>gi|6940719|gb|AAF31753.1| (AF087937) melanocortin-4 receptor MC4R [Sus scrofa]  
 Length = 248

Score = 389 bits (1000), Expect = e-107  
 Identities = 228/248 (91%), Positives = 228/248 (91%)

Query: 73 KNLHSPMYFFICSLAVADMLVSVSNGSETIVITLLNSTDTDAQSFTVNIDNVIDXXXXX 132  
 KNLHSPMYFFICSLAVADMLVSVSNGSETIVITLLNSTDTDAQSFTVNIDNVID  
 Sbjct: 1 KNLHSPMYFFICSLAVADMLVSVSNGSETIVITLLNSTDTDAQSFTVNIDNVIDSVICSS 60

Query: 133 XXXXXXXXXXXXXXXRYFTIFYALQYHNIMTVKRVGIIISCIWAVCTVSGVLFIISDSSA 192  
 DRYFTIFYALQYHNIMTVKRVGIIISCIWAVCTVSGVLFIISDSSA  
 Sbjct: 61 LLASICSLLSIAVDYFTIFYALQYHNIMTVKRVGIIISCIWAVCTVSGVLFIISDSSA 120

Query: 193 VIICLITVFFTMLALMASLYVHMFLMARLHIKRIAVLPGTG TIRQGANMKGAITLTILIG 252  
 VIICLITVFFTMLALMASLYVHMFLMARLHIKRIAVLPGTG TIRQGANMKGAITLTILIG  
 Sbjct: 121 VIICLITVFFTMLALMASLYVHMFLMARLHIKRIAVLPGTG TIRQGANMKGAITLTILIG 180

Query: 253 VFVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPLIYALRSQELRKT 312  
VFVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSII PLIYALRSQELRKT  
Sbjct: 181 VFVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIXPLIYALRSQELRKT 240

Query: 313 FKEIICCY 320  
FKEIICCY

Sbjct: 241 FKEIICCY 248

>gi|3061273|dbj|BAA25640.1| (AB012868) melanocortin 5-receptor [Gallus gallus]  
Length = 325

Score = 339 bits (869), Expect = 2e-92

Identities = 199/317 (62%), Positives = 241/317 (75%), Gaps = 5/317 (1%)

Query: 17 NRSTYGLHSNASEPLGKGYSEGGCYEQLFVSPEVFTLGVISLLENILVIVAIKKNLH 76  
N S +G SN + P K S+ EQ+ ++ EVF+ LG++SLLLENILVI AI KKNLH  
Sbjct: 13 NLSAFG--SNFTVPTVK--SKSSPCEQVVIAAEVFLILGIVSLLLENILVICAIVKKNLH 68

Query: 77 SPMYFFICSLAVADMLVSVSNGSETIVITLLNSTDTDAQ-SFTVNIDNVIDXXXXXXXXX 135  
SPMYFF+CSLAVADMLVSVSN ETI I L+N+ + +F +IDNV D  
Sbjct: 69 SPMYFFVCSLAVADMLVSVSNAWETITITYLINNRHIIMEDAFVRHIDNVFDSLICISVVA 128

Query: 136 XXXXXXXXXXXDRYFTIFYALQYHNIMTVKRVGIIISCIWAVCTVSGVLFIIYSDSSAVII 195  
DRY TIFYAL+YHNIMTVKR G+II+CIW CT G++FI+Y +S+ VII  
Sbjct: 129 SMCSLLAIAVDRIYITIFYALRYHNIMTVKRSGLIIACIWTFTCTGCGIIFILYESTYVII 188

Query: 196 CLITVFFTMLALMASLYVHMFLMARLHIKRIAVLPGTGTIRQGANMKGAITLTILIGVFV 255  
CLIT+FFTML LM SLY+HMFL+AR H+K+IA LPG ++ Q +MKGAITLT+L+G+F+  
Sbjct: 189 CLITMFFTMLFLMVSLYIHMFLRLARTHVKKIAALPGYNSVHQRTSMKGAITLTMLLGIFI 248

Query: 256 VCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPLIYALRSQELRKT FKE 315  
VCWAPFFLHLI ISCPQN YCVCFMSHFN+YLILIMCNS+IDPLIYA RSQE+RKT FKE  
Sbjct: 249 VCWAPFFLHLILMISCPQNLVYCVCFMSHFNMYLILIMCNSVIDPLIYAFRSQEMRKT FKE 308

Query: 316 IICCYPLGGLCDLSSRY 332  
IICCY + +C LS++Y  
Sbjct: 309 IICCYSVRMVCGLSNKY 325

>gi|7305263|ref|NP\_038624.1| melanocortin 5 receptor [Mus musculus]  
gi|2137511|pir|I49008 melanocortin-5 receptor - mouse  
gi|522166|gb|AAA76585.1| (U08354) melanocortin-5 receptor [Mus musculus]  
Length = 372

Score = 333 bits (854), Expect = 1e-90

Identities = 178/292 (60%), Positives = 220/292 (74%), Gaps = 1/292 (0%)

Query: 42 EQLFVSPEVFTLGVISLLENILVIVAIKKNLHSPMYFFICSLAVADMLVSVSNGSET 101  
E++ ++ EVF+TLG++SLLLENILVI AI KKNLHSPMYF++ SLAVADMLVS+SN ET  
Sbjct: 81 EEMGIAVEVFTLGLVSLLENILVIGAIVKKNLHSPMYFYVGLAVADMLVSMSNAWET 140

Query: 102 IVITLLNSTD-TDAQSFTVNIDNVIDXXXXXXXXXXXXXXXXXXXXRYFTIFYALQYHNI 160  
+ I LLN+ A +F +IDNV D DRY TIFYAL+YH+I  
Sbjct: 141 VTIYLLNNKHLVIADTFVRHIDNVFDSMICISVVASMCSLLAIAVDRIYITIFYALRYHHI 200

Query: 161 MTVKRVGIIISCIWAVCTVSGVLFIIYSDSSAVIICLITVFFTMLALMASLYVHMFLMAR 220  
MT +R G+II+CIW C G++FIIY +S VIICLI++FFTML M SLY+HMFL+AR

Sbjct: 201 MTARRSGVIIACIWTFCISC GIVFIIYYESKYVIIICLISMFFTMLFFMVSLYIHMFLAR 260

Query: 221 LHIKRIAVLP GTGTIRQGANMKGAILTLILIGVFVVCWAPFFLHLIFYISCPQN PYCVCF 280  
H+KRIA P ++RQ +MKGAILTL+L+G+F+VCW+PFFLHLI ISCPQN YC CF

Sbjct: 261 NHVKRIAASPRYNSVRQRTSMKGAILTLM LGIFIVCWSPFFLHLILMISCPQNVYCSCF 320

Query: 281 MSHFNLYLILIMCNSIIDPLIYALRSQELRKT FKEIICCYPLGGLCDLSSRY 332  
MS+FN+YLILIMCNS+IDPLIYALRSQE+R+TFKEI+CC+ C L Y

Sbjct: 321 MSYFNMYLILIMCNSVIDPLIYALRSQEMRRT FKEIVCCHGFRRPCRLGGY 372

>gi|13629514|sp|Q9TT23|MC5R\_PANTR MELANOCORTIN-5 RECEPTOR (MC5-R)  
gi|6625968|gb|AAF19441.1|AF208691\_1 (AF208691) melanocortin 5 receptor [Pan troglod  
Length = 325

Score = 325 bits (834), Expect = 2e-88  
Identities = 191/332 (57%), Positives = 232/332 (69%), Gaps = 9/332 (2%)

Query: 1 MNSTHHHGMHTSLHFWNRSTYGLHSNASEPLGKG YSEGGCYEQLFVSPEVFVTLGVISLL 60  
MNS+ H LHF + + N S P K S E + ++ EVF+TLGVISLL

Sbjct: 1 MNSSFH-----LHFLDLNLNATEGNLSGPNVKNKSSP--CEDMGIAVEVFLTLGVISLL 52

Query: 61 ENILVIVAI AKNKNLHSPMYFFICSLAVADMLVSVSNGSETIVITLLNSTD-TDAQSFTV 119  
ENILVI AI KNKNLHSPMYFF+CSLAVADMLVS+S+ ETI I LLN+ A +F

Sbjct: 53 ENILVIGAIVKNKNLHSPMYFFVCSLAVADMLVSMSSAWETIT IYLLNNKHLVIADAFVR 112

Query: 120 NIDNVIDXXXXXXXXXXXXXXXXXXXXDRYFTIFYALQYHNIMTVKRVGIIISCIWAVCTV 179  
+IDNV D DRY TIFYAL+YH+IMT +R G II+ IWA CT

Sbjct: 113 HIDNVFDSMICISVVASMCSSLAI AVDRYVTIFYALRYHHIMTARRSGAIIAGIWAFACTG 172

Query: 180 SGVLFIIYSDSSAVIICLITVFFTMLALMASLYVHMFLMARLHIKRIAVLP GTGTIRQGA 239  
G++FI+YS+S+ VI+CLI++FF ML L+ SLY+HMFL+AR H+KRIA LP + RQ

Sbjct: 173 CGIVFILYSESTYVILCLISMFFAMFLLLVSLYIHMFL LARTHVKRIAALPRASSARQRT 232

Query: 240 NMKGAILTLILIGVFVVCWAPFFLHLIFYISCPQN PYCVCFMSHFNLYLILIMCNSIIDP 299  
+M+GA+T+T+L+GVF VCWAPFFLHL +SCPQN YC CFMSHFN+YLILIMCNS++DP

Sbjct: 233 SMQGA VTM L LGVFTVCWAPFFLHLTLMLSCPQNLYCSCFMSHFNMYLILIMCNSVMDP 292

Query: 300 LIYALRSQELRKT FKEIICCYPLGGLCDLSSR 331  
LIYA RSQE+RKT FKEIICC C R

Sbjct: 293 LIYAFRSQEMRKT FKEIICCRGFRIACSFPRR 324

>gi|5174535|ref|NP\_005904.1| melanocortin 5 receptor [Homo sapiens]  
gi|11424009|ref|XP\_008685.1| melanocortin 5 receptor [Homo sapiens]  
gi|729996|sp|P33032|MC5R\_HUMAN MELANOCORTIN-5 RECEPTOR (MC5-R) (MC-2)  
gi|522164|gb|AAB60376.1| (U08353) melanocortin-5 receptor [Homo sapiens]  
gi|939925|emb|CAA80962.1| (Z25470) melanocortin receptor [Homo sapiens]  
Length = 325

Score = 325 bits (833), Expect = 3e-88  
Identities = 191/332 (57%), Positives = 232/332 (69%), Gaps = 9/332 (2%)

Query: 1 MNSTHHHGMHTSLHFWNRSTYGLHSNASEPLGKG YSEGGCYEQLFVSPEVFVTLGVISLL 60  
MNS+ H LHF + + N S P K S E + ++ EVF+TLGVISLL

Sbjct: 1 MNSSFH-----LHFLDLNLNATEGNLSGPNVKNKSSP--CEDMGIAVEVFLTLGVISLL 52

Query: 61 ENILVIVAI AKNKNLHSPMYFFICSLAVADMLVSVSNGSETIVITLLNSTD-TDAQSFTV 119

ENILVI AI KNKNLHSPMYFF+CSLAVADMLVS+S+ ETI I LLN+ A +F  
 Sbjct: 53 ENILVIGAIVKNKNLHSPMYFFVCSLAVADMLVSMSSAWETITITYLLNNKHLVIADAFVR 112  
 Query: 120 NIDNVIDXXXXXXXXXXXXXXXXXXXXDRYFTIFYALQYHNIMTVKRVGIIISCIWAVCTV 179  
 +IDNV D DRY TIFYAL+YH+IMT +R G II+ IWA CT  
 Sbjct: 113 HIDNVFDSMICISVVASMCSLLAIAVDRYVTIFYALRYHHIMTARRSGAIIAGIWAFACTG 172  
 Query: 180 SGVLFIISDSSAVIICLITVFFTMLALMASLYVHMFLMARLHIKRIAVLPGTGTIRQGA 239  
 G++FI+YS+S+ VI+CLI++FF ML L+ SLY+HMFL+AR H+KRIA LPG + RQ  
 Sbjct: 173 CGIVFILYSESTYVILCLISMFFAMFLLLVSLYIHMFLARTHVKRIAALPGASSARQRT 232  
 Query: 240 NMKGAITLTILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFMESHFNLYLILIMCNSIIDP 299  
 +M+GA+T+T+L+GVF VCWAPFFLHL +SCPQN YC FMSHFN+YLILIMCNS++DP  
 Sbjct: 233 SMQGAVTVTMLLGVFTVCWAPFFLHLTLMLSCPQNLYCSRFSHFNMYLILIMCNSVMDP 292  
 Query: 300 LIYALRSQELRKTFKEIICCYPLGGLCDLSSR 331  
 LIYA RSQE+RKTFKEIICC C R  
 Sbjct: 293 LIYAFRSQEMRKTFKEIICCRGFRIACSFPRR 324

>gi|7447148|pir|JC5592 melanocortin 5 receptor - human  
 gi|435600|qb|AAA59566.1| (L27080) melanocortin 5 receptor [Homo sapiens]  
 Length = 325

Score = 324 bits (830), Expect = 8e-88

Identities = 191/332 (57%), Positives = 231/332 (69%), Gaps = 9/332 (2%)

Query: 1 MNSTHHHGMHTSLHFVNRSTYGLHSNASEPLGKGYSEGGCYEQLFVSPEVFTLGVISLL 60  
 MNS+ H LHF + + N S P K S E + ++ EVF+TLGVISLL  
 Sbjct: 1 MNSSFH-----LHFLDLNLNATEGNLSGPNVKNKSSP--CEDMGIAVEVFLTLGVISLL 52  
 Query: 61 ENILVIVAIKKNKNLHSPMYFFICSLAVADMLVSVSNGSETIVITLLNSTD-TDAQSFTV 119  
 ENILVI AI KNKNLHSPMYFF+CSLAVADMLVS+S+ ETI I LLN+ A +F  
 Sbjct: 53 ENILVIGAIVKNKNLHSPMYFFVCSLAVADMLVSMSSAWETITITYLLNNKHLVIADAFVR 112  
 Query: 120 NIDNVIDXXXXXXXXXXXXXXXXXXXXDRYFTIFYALQYHNIMTVKRVGIIISCIWAVCTV 179  
 +IDNV D DRY TIFYAL YH+IMT +R G II+ IWA CT  
 Sbjct: 113 HIDNVFDSMICISVVASMCSLLAIAVDRYVTIFYALAYHHIMTARRSGAIIAGIWAFACTG 172  
 Query: 180 SGVLFIISDSSAVIICLITVFFTMLALMASLYVHMFLMARLHIKRIAVLPGTGTIRQGA 239  
 G++FI+YS+S+ VI+CLI++FF ML L+ SLY+HMFL+AR H+KRIA LPG + RQ  
 Sbjct: 173 CGIVFILYSESTYVILCLISMFFAMFLLLVSLYIHMFLARTHVKRIAALPGASSARQRT 232  
 Query: 240 NMKGAITLTILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFMESHFNLYLILIMCNSIIDP 299  
 +M+GA+T+T+L+GVF VCWAPFFLHL +SCPQN YC FMSHFN+YLILIMCNS++DP  
 Sbjct: 233 SMQGAVTVTMLLGVFTVCWAPFFLHLTLMLSCPQNLYCSRFSHFNMYLILIMCNSVMDP 292  
 Query: 300 LIYALRSQELRKTFKEIICCYPLGGLCDLSSR 331  
 LIYA RSQE+RKTFKEIICC C R  
 Sbjct: 293 LIYAFRSQEMRKTFKEIICCRGFRIACSFPRR 324

>gi|6981190|ref|NP\_037314.1| melanocortin 5 receptor [Rattus norvegicus]  
 gi|547899|sp|P35345|MC5R\_RAT MELANOCORTIN-5 RECEPTOR (MC5-R)  
 gi|628005|pir|JC2193 melanocortin receptor, MC5 - rat  
 gi|435607|qb|AAA41577.1| (L27081) melanocortin 5 receptor [Rattus norvegicus]  
 Length = 325

Score = 322 bits (825), Expect = 3e-87  
 Identities = 191/328 (58%), Positives = 237/328 (72%), Gaps = 7/328 (2%)

Query: 9 MHTSLHFWRNSTYGLHSNASEP--LGKGY-SEGGCYEQLFVSPEVFTVLGVISLLENILV 65  
 M++S H + L NASE LG+ ++ E + ++ EVF+TLG++SLLLENILV  
 Sbjct: 1 MNSSSHL---TLLDLTLNASEDNILGQNVNNKSSACEDMGIAVEVFTLTGLVSLLENILV 57

Query: 66 IVAIAKNKNLHSPMYFFICSLAVADMLVSVSNGSETIVITLLNSTD-TDAQSFTVNIDNV 124  
 I AI KNKNLHSPMYFF+ SLAVADMLVS+SN ETI I L+N+ A +F +IDNV  
 Sbjct: 58 IGAIVKNKNLHSPMYFFVGS LAVADMLVSMNAWETITITYLINNKHVVIADTFVRHIDNV 117

Query: 125 IDXXXXXXXXXXXXXXXXXXXXRYFTIFYALQYHNIMTVKRVGIIISCIWAVCTVSGVLF 184  
 D DRY TIFYAL+YH+IMT +R G+II+CIW C G++F  
 Sbjct: 118 FDSMICISVVASMCSLLAIAVDRIYITIFYALRYHHIMTARRSGVIIACIWTFCISCGIVF 177

Query: 185 IIYSDSSAVIICLITVFFTMLALMASLYVHMFLMARLHIKRIAVLPGTGTIRQGANMKGA 244  
 IIY +S VI+CLI++FFTML M SLY+HMFL+AR H+KRIA P ++RQ A+MKGA  
 Sbjct: 178 IIYESKYVIVCLISMFFTMLFFMVSLYIHMFLARNHVKRIAASPRYNSVRQRASMKGA 237

Query: 245 ITLTILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPLIYAL 304  
 ITLT+L+G+F+VCW+PFFLHLI ISCPQN YC CFMS+FN+YLILIMCNS+IDPLIYAL  
 Sbjct: 238 ITLTMLLGIFIVCWSPFFLHLILMISCPQNVYCACFMSYFNMYLILIMCNSVIDPLIYAL 297

Query: 305 RSQELRKTFKEIICCYPLGGLCDLSSRY 332  
 RSQE+R+TFKEIICC+ C L RY  
 Sbjct: 298 RSQEMRRTFKEIICCHGFRRTCTLLGRY 325

>gi|729997|sp|P41149|MC5R\_MOUSE MELANOCORTIN-5 RECEPTOR (MC5-R)  
 gi|498974|emb|CAA53943.1| (X76295) melanocortin 5 receptor [Mus musculus]  
 Length = 325

Score = 320 bits (819), Expect = 1e-86  
 Identities = 179/292 (61%), Positives = 220/292 (75%), Gaps = 1/292 (0%)

Query: 42 EQLFVSPEVFTVLGVISLLENILVIVAIAKNKNLHSPMYFFICSLAVADMLVSVSNGSET 101  
 E++ ++ EVF+TLG++SLLLENILVI AI KNKNLHSPMYFF+ SLAVADMLVS+SN ET  
 Sbjct: 34 EEMGIAVEVFTLTGLVSLLENILVIGAIVKNKNLHSPMYFFVGS LAVADMLVSMNAWET 93

Query: 102 IVITLLNSTD-TDAQSFTVNIDNVIDXXXXXXXXXXXXXXXXXXXXRYFTIFYALQYHNI 160  
 + I LLN+ A +F +IDNV D DRY TIFYAL+YH+I  
 Sbjct: 94 VTIYLLNNKHLVIADTFVRHIDNVFDSMICISVVASMCSLLAIAVDRIYITIFYALRYHHI 153

Query: 161 MTVKRVGIIISCIWAVCTVSGVLFIIYSDSSAVIICLITVFFTMLALMASLYVHMFLMAR 220  
 MT +R G+II+CIW C G++FIIY +S VIICLI++FFTML M SLY+HMFL+AR  
 Sbjct: 154 MTARRSGVIIACIWTFCISCGIVFIIYESKYVIICLISMFFTMLFFMVSLYIHMFLAR 213

Query: 221 LHIKRIAVLPGTGTIRQGANMKGAITLTILIGVFVVCWAPFFLHLIFYISCPQNPYCVCF 280  
 H+KRIA P ++RQ +MKGAITLT+L+G+F+VCW+PFFLHLI ISCPQN YC CF  
 Sbjct: 214 NHVKRIAASPRYNSVRQRTSMKGAITLTMLLGIFIVCWSPFFLHLILMISCPQNVYCSCF 273

Query: 281 MSHFNLYLILIMCNSIIDPLIYALRSQELRKTFKEIICCYPLGGLCDLSSRY 332  
 MS+FN+YLILIMCNS+IDPLIYALRSQE+R+TFKEI+CC+ C L Y  
 Sbjct: 274 MSYFNMYLILIMCNSVIDPLIYALRSQEMRRTFKEIVCCHGFRRPCRLGGY 325

>gi|468378|gb|AAA21337.1| (L22527) melanocortin-5 receptor [Mus sp.]  
 Length = 325

Score = 318 bits (816), Expect = 3e-86

Identities = 178/292 (60%), Positives = 220/292 (74%), Gaps = 1/292 (0%)

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Query: 42  EQLFVSPEVFTLGLVISLLENILVIVAIKKNLHSPMYFFICSLAVADMLVSVSNGSET 101
          E++ ++ EVF+TLG++SLLLENILVI AI KNKNLHSPMYF++ SLAVADMLVS+SN ET
Sbjct: 34  EEMGIAVEVFTLGLVSLLENILVIGAIVKKNLHSPMYFYVGS LAVADMLVSM SNAWET 93

Query: 102 IVITLLNSTD-TDAQSFTVNIDNVIDXXXXXXXXXXXXXXXXXXXXRYFTIFYALQYHNI 160
          + I LLN+      A +F +IDNV D                      DRY TIFYAL+YH+I
Sbjct: 94  VTIIYLLNNKHLVIADTFVRHIDNVFDSMICISVVASMCSSLAIADVRYITIFYALRYHHI 153

Query: 161 MTVKRVGIIISCIWAVCTVSGVLFIIYSDSSAVIICLITVFFTMLALMASLYVHMFLMAR 220
          MT +R G+II+CIW C   G++FIIY +S VIICLI++FFTML M SLY+HMFL+AR
Sbjct: 154 MTARRSGVIIACIWTFCISCIGVFIYYESKYVIIICLISMFFTMLFFMVSLYIHMFLAR 213

Query: 221 LHIKRIAVLPGTGTIRQGANMKGAITLTILIGVFVVCWAPFFLHLIFYISCPQNPYCVCF 280
          H+KRIA P   ++RQ +MKGAITLT+L+G+F+VCW+PFFLHLI ISCPQN YC CF
Sbjct: 214 NHVKRIAASPRYNSVRQRTSMKGAITLTMLLGIFIVCWSPFFLHLILMISCPQNVYCSCF 273

Query: 281 MSHFNLYLILIMCNSIIDPLIYALRSQELRKTFKEIICCYPLGGLCDLSSRY 332
          MS+FN+YLILIMCNS+IDPLIYALRSQE+R+TFKEI+CC+      C L   Y
Sbjct: 274 MSYFNMYLILIMCNSVIDPLIYALRSQEMRRTFKEIVCCHGFRRPCRLGGY 325

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>gi|627524|pir|JN0764 melanocortin receptor 2 - human  
Length = 325

Score = 318 bits (816), Expect = 3e-86

Identities = 188/332 (56%), Positives = 229/332 (68%), Gaps = 9/332 (2%)

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Query: 1  MNSTHHHGMHTSLHFWNRSTYGLHSNASEPLGKGYSEGGCYEQLFVSPEVFTLGLVISLL 60
          MNS+ H      LHF + +      N S P K S      E + ++ EVF+TLGLVISLL
Sbjct: 1  MNSSFH-----LHFLDLNLNATEGNLSGPNVKNKSSP--CEDMGIAVEVFTLGLVISLL 52

Query: 61  ENILVIVAIKKNLHSPMYFFICSLAVADMLVSVSNGSETIVITLLNSTD-TDAQSFTV 119
          ENILVI AI KNKNLHSPMYFF+CSLAVADMLVS+S+ ETI I LLN+      A +F
Sbjct: 53  ENILVIGAIVKKNLHSPMYFFVCSLAVADMLVSMSSAWETITIIYLLNNKHLVIADAFVR 112

Query: 120 NIDNVIDXXXXXXXXXXXXXXXXXXXXRYFTIFYALQYHNIMTVKRVGIIISCIWAVCTV 179
          +IDNV D                      DRY TIFYAL+YH+IMT +R G II+ IWA CT
Sbjct: 113 HIDNVFDSMICISVVASMCSSLAIADVRYVTIFYALRYHHIMTARRSGAIIAGIWAFCTG 172

Query: 180 SGVLFIIYSDSSAVIICLITVFFTMLALMASLYVHMFLMARLHIKRIAVLPGTGTIRQGA 239
          G++FI+YS+S+ VI+CLI++FF ML L+ SLY+HMFL+AR H+KRIA+ PG      +G
Sbjct: 173 CGIVFILYSESTYVILCLISMFFAMFLLVSLYIHMFLLARTHVKRIALCPGPALRGRGP 232

Query: 240 NMKGAITLTILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDP 299
          +GA+T+T+L+GVF VCWAPFFLHL +SCPQN YC FMSHFN+YLILIMCNS++DP
Sbjct: 233 AWQGAVTVTMLLGVFTVCWAPFFLHLTLMLSCPQNLYCSRFSHFNMYLILIMCNSVMDP 292

Query: 300 LIYALRSQELRKTFKEIICCYPLGGLCDLSSR 331
          LIYA RSQE+RKTFKEIICC      C      R
Sbjct: 293 LIYAFRSQEMRKTFKEIICCRGFRIACSFPRR 324

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>gi|1363304|pir|B57055 melanocortin-4 receptor - rat (fragment)  
Length = 215

Score = 317 bits (811), Expect = 1e-85  
Identities = 187/215 (86%), Positives = 191/215 (87%)

Query: 78 PMYFFICSLAVADMLVSVSNGSETIVITLLNSTDTDAQSFTVNIDNVIDXXXXXXXXXXXX 137  
PMYFFICSLAVADMLVSVSNGS +IVITLLNSTDTDAQSFTVNIDNVID  
Sbjct: 1 PMYFFICSLAVADMLVSVSNGSVSIVITLLNSTDTDAQSFTVNIDNVIDSVICSSLLASI 60

Query: 138 XXXXXXXXDRYFTIFYALQYHNIMTVKRVGIIISCIWAVCTVSGVLFIIYSDSSAVIICL 197  
DRYFTIFYALQYHNIMTV+RVGIIISCIWA CTVSGVLFIIYSDSSAVIICL  
Sbjct: 61 CSLLSIAVDYFTIFYALQYHNIMTVRRVGIIISCIWAACCTVSGVLFIIYSDSSAVIICL 120

Query: 198 ITVFFTMLALMASLYVHMFLMARLHIKRIAVLPGTGTIRQGANMKGAITLTILIGVFVVC 257  
IT+FFTML LMASLYVHMFLMARLHIKRIAVLPGTG IRQGANMKG ITLTILIGVFVVC  
Sbjct: 121 ITMFFTMLVLMAVLYVHMFLMARLHIKRIAVLPGTGAIQGANMKGITLTILIGVFVVC 180

Query: 258 WAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIM 292  
WAPFFLHL+FYISCPQNPYCVCFMSHFNLYLILIM  
Sbjct: 181 WAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIM 215

>gi|422989|pir|B46647 melanocortin receptor 3 - human  
gi|299419|gb|AAB26088.1| melanocortin-3 receptor [human, Peptide, 360 aa]  
Length = 360

Score = 309 bits (792), Expect = 2e-83  
Identities = 167/292 (57%), Positives = 213/292 (72%), Gaps = 3/292 (1%)

Query: 30 PLGKGYSEGGCYEQLFVSPEVFVTLGVISLLENILVIVAIKKNLHSPMYFFICSLAVA 89  
P S EQ+F+ PE+F++LG++SLLLENILVI+A+ +N NLHSPMYFF+CSLAVA  
Sbjct: 61 PFFSNQSSSAFCEQVFIKPEIFLSLGIVSLLLENILVILAVVRNGLHSPMYFFLCSLAVA 120

Query: 90 DMLVSVSNGSETIVITLLNSTD-TDAQSFTVNIDNVIDXXXXXXXXXXXXXXXXXXXXRY 148  
DMLVSVSN ETI+I +++S D T F ++DN+ D DRY  
Sbjct: 121 DMLVSVSNALETIMIAIVHSDDYTFEDQFIQHMDNIFDSMICISLVASICNLLAIAVDY 180

Query: 149 FTIFYALQYHNIMTVKRVGIIISCIWAVCTVSGVLFIIYSDSSAVIICLITVFFTMLALM 208  
TIFYAL+YH+IMTV++ +I IW C V GV+FI+YS+S VI+CLIT+FF M+ LM  
Sbjct: 181 VTIFYALRYHSIMTVRKALTLIVAIWCCGVCVGVFIVYSESKMVIVCLITMFFAMMLLM 240

Query: 209 ASLYVHMFLMARLHIKRIAVLPGTGTI--RQGANMKGAITLTILIGVFVVCWAPFFLHLI 266  
+LYVHMFL ARLH+KRIA LP + +Q + MKGA+T+TIL+GVF+ CWAPFFLHL+  
Sbjct: 241 GTLYVHMFLFARLHVKRIAALPPADGVAPQHQHSCMKGAVTITILLGVFIFCWAPFFLHLV 300

Query: 267 FYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPLIYALRSQELRKTKEIIC 318  
I+CP NPYC C+ +HFN YL+LIMCNS+IDPLIYA RS ELR TF+EI+C  
Sbjct: 301 LIITCPTNPYCTCYTAHFNTYLVLMCNSVIDPLIYAFRSLRLRNTFREILC 352

>gi|6678822|ref|NP\_032587.1| melanocortin 3 receptor [Mus musculus]  
gi|417278|sp|P33033|MC3R\_MOUSE MELANOCORTIN-3 RECEPTOR (MC3-R)  
gi|1083412|pir|S43850 melanocortin 3 receptor - mouse  
gi|400474|emb|CAA52918.1| (X74983) melanocortin 3 receptor [Mus musculus]  
Length = 323

Score = 307 bits (787), Expect = 7e-83  
Identities = 168/299 (56%), Positives = 217/299 (72%), Gaps = 3/299 (1%)

Query: 23 LHSNASEPLGKGYSSEGGCYEQLFVSPEVFTLGVISLLENILVIVAIKKNLHSPMYFF 82  
 L + + P S G EQ+F+ PEV+ LG++SL+ENILVI+A+ +N NLHSPMYFF  
 Sbjct: 17 LSEHPAAPPASNRSGSGFCEQVFIKPEVFLALGIVSLMENILVILAVVRNGLHSPMYFF 76

Query: 83 ICSLAVADMLVSVSNGSETIVITLLNSTD-TDAQSFTVNIDNVIDXXXXXXXXXXXXXXXXX 141  
 +CSLA ADMLVS+SN ETI+I ++NS T F ++DN+ D  
 Sbjct: 77 LCSLAAADMLVSLSNSLETIMIAVINSDSLTLEDQFIQHMDNIFDSMICISLVASICNLL 136

Query: 142 XXXXDRIYFTIFYALQYHNIMTVKRVGIIISCIWAVCTVSGVLFIIYSDSSAVIICLITVF 201  
 DRY TIFYAL+YH+IMTV++ +I IW C + GV+FIIYS+S VI+CLIT+F  
 Sbjct: 137 AIAIDRYVTIFYALRYHSIMTVRKALTLIGVIWCCGICGVMFIIYSESKMVIVCLITMF 196

Query: 202 FTMLALMASLYVHMFLMARLHIKRIAVLPGTGTI--RQGANMKGAITLTILIGVFVVCWA 259  
 F M+ LM +LY+HMFL ARLH++RIAVLP G + +Q + MKGA+T+TIL+GVF+ CWA  
 Sbjct: 197 FAMVLLMGTLYIHMFLFARLHVQRIAVLPAGVVPQGHSCMKGAVTITILLGVFIFCWA 256

Query: 260 PFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPLIYALRSQELRKTTFKEIIC 318  
 PFFLHL+ I+CP NPYC+C+ +HFN YL+LIMCNS+IDPLIYA RS ELR TFKEI+C  
 Sbjct: 257 PFFLHLVLIITCPTNPYICICYTAHFNTYLVLMCNSVIDPLIYAFRSLELRNTFKEILC 315

>gi|3493361|dbj|BAA32555.1| (AB017137) melanocortin 3-receptor [Gallus gallus]  
 Length = 325

Score = 307 bits (787), Expect = 7e-83

Identities = 181/285 (63%), Positives = 213/285 (74%), Gaps = 2/285 (0%)

Query: 36 SEGGCYEQLFVSPEVFTLGVISLLENILVIVAIKKNLHSPMYFFICSLAVADMLVSV 95  
 S+G C EQ+F+ EVF+TLG+ISL+ENILVI+A+ KN NLHSPMYFF+CSLAVADMLVS  
 Sbjct: 31 SDGFC-EQVFIKAEVFLTLGIISLMENILVILAVLKNGLHSPMYFFLCSLAVADMLVST 89

Query: 96 SNGSETIVITLLNSTDTDAQS-FTVNIDNVIDXXXXXXXXXXXXXXXXXXDRYFTIFYA 154  
 SN ETI+I +L+S F ++DNV D DRY TIFYA  
 Sbjct: 90 SNALETIMIAILSSGYLIIDDHFIQHMDNVFDSMICISLVASICNLLVIAIDRYITIFYA 149

Query: 155 LQYHNIMTVKRVGIIISCIWAVCTVSGVLFIIYSDSSAVIICLITVFFTMLALMASLYVH 214  
 L YH+IMTVK+ +I IW C + G++FI YS+S VI+CLIT+FFTML LMASLYVH  
 Sbjct: 150 LLYHSIMTVKKALTIVLIVLWISCIICGIIIFAYSESKTVIVCLITMFFTMLFLMASLYVH 209

Query: 215 MFLMARLHIKRIAVLPGTGTIRQGANMKGAITLTILIGVFVVCWAPFFLHLIFYISCPQN 274  
 MFL ARLH+KRIA LP G Q MKGAIT+TIL+GVF+VCWAPFFLHLI ISCP N  
 Sbjct: 210 MFLFARLHVKRIAALPVDGVPSQRTCMKGAITITILLGVFIVCWAPFFLHLILIISCPMN 269

Query: 275 PYCVCFMSHFNLYLILIMCNSIIDPLIYALRSQELRKTTFKEIICC 319  
 PYCVC+ SHFN YL+LIMCNS+IDPLIYA RS E+RKTTFKEI+CC  
 Sbjct: 270 PYCVCYTSHFNTYLVLMCNSVIDPLIYAFRSLEMRKTTFKEIVCC 314

>gi|9845271|ref|NP\_063941.1| melanocortin 3 receptor [Homo sapiens]  
 gi|1170883|sp|P41968|MC3R\_HUMAN MELANOCORTIN-3 RECEPTOR (MC3-R)  
 gi|188674|gb|AAC13541.1| (L06155) melanocortin receptor [Homo sapiens]  
 Length = 360

Score = 306 bits (784), Expect = 2e-82

Identities = 166/292 (56%), Positives = 213/292 (72%), Gaps = 3/292 (1%)

Query: 30 PLGKGYSSEGGCYEQLFVSPEVFTLGVISLLENILVIVAIKKNLHSPMYFFICSLAVA 89  
 P S EQ+F+ PE+F++LG++SLLLENILVI+A+ +N NLHSPMYFF+CSLAVA



Sbjct: 61 PFFSNQSSSAFCEQVFIKPEIFLSLIGVSLLENILVILAVVRNGNLHSPMYFFFLCSLAVA 120

Query: 90 DMLVSVSNGSETIVITLLNSTD-TDAQSFTVNIDNVIDXXXXXXXXXXXXXXXXXXXXRY 148  
 DMLVSVSN ETI+I +++S T F ++DN+ D DRY

Sbjct: 121 DMLVSVSNALETIMIAIVHSDYLTFFEDQFIQHMDNIFDSMICISLVASICNLLAIAVDRY 180

Query: 149 FTIFYALQYHNIMTVKRVGIIISCIWAVCTVSGVLFIIYSDSSAVIICLITVFFTMLALM 208  
 TIFYAL+YH+IMTV++ +I IW C V GV+FI+YS+S VI+CLIT+FF M+ LM

Sbjct: 181 VTIFYALRYHSIMTVRKALTLIVAIWCCGVCVGFIVYSESKMVIVCLITMFFAMMLLM 240

Query: 209 ASLYVHMFLMARLHIKRIAVLPGTGTI--RQGANMKGAITLTILIGVFVVCWAPFFLHLI 266  
 +LYVHMFL ARLH+KRIA LP + +Q + MKGA+T+TIL+GVF+ CWAPFFLHL+

Sbjct: 241 GTLYVHMFLFARLHVKRIAALPPADGVAPQQHSCMKGAVTITILLGVFIFCWAPFFLHLV 300

Query: 267 FYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPLIYALRSQELRKTFKEIIC 318  
 I+CP NPYC+C+ +HFN YL+LIMCNS+IDPLIYA RS ELR TF+EI+C

Sbjct: 301 LIITCPTNPYCICYTAHFNTYLVLMCNSVIDPLIYAFRSLELRNTFREILC 352

>gi|11420991|ref|XP\_009545.1| melanocortin 3 receptor [Homo sapiens]  
 gi|11125637|emb|CAC15480.1| (AL139824) bA380D15.1 (melanocortin 3 receptor) [Homo s]  
 Length = 360

Score = 306 bits (784), Expect = 2e-82  
 Identities = 167/292 (57%), Positives = 213/292 (72%), Gaps = 3/292 (1%)

Query: 30 PLGKGYSEGGCYEQLFVSPEVFVTLGVISLLENILVIVAIKKNLHSPMYFFICSLAVA 89  
 P S EQ+F+ PEVF++LG++SLENILVI+A+ +N NLHSPMYFF+CSLAVA

Sbjct: 61 PFFSNQSSSAFCEQVFIKPEVFLSLIGVSLLENILVILAVVRNGNLHSPMYFFFLCSLAVA 120

Query: 90 DMLVSVSNGSETIVITLLNSTD-TDAQSFTVNIDNVIDXXXXXXXXXXXXXXXXXXXXRY 148  
 DMLVSVSN ETI+I +++S T F ++DN+ D DRY

Sbjct: 121 DMLVSVSNALETIMIAIVHSDYLTFFEDQFIQHMDNIFDSMICISLVASICNLLAIAVDRY 180

Query: 149 FTIFYALQYHNIMTVKRVGIIISCIWAVCTVSGVLFIIYSDSSAVIICLITVFFTMLALM 208  
 TIFYAL+YH+IMTV++ +I IW C V GV+FI+YS+S VI+CLIT+FF M+ LM

Sbjct: 181 VTIFYALRYHSIMTVRKALTLIVAIWCCGVCVGFIVYSESKMVIVCLITMFFAMMLLM 240

Query: 209 ASLYVHMFLMARLHIKRIAVLPGTGTI--RQGANMKGAITLTILIGVFVVCWAPFFLHLI 266  
 +LYVHMFL ARLH+KRIA LP + +Q + MKGA+T+TIL+GVF+ CWAPFFLHL+

Sbjct: 241 GTLYVHMFLFARLHVKRIAALPPADGVAPQQHSCMKGAVTITILLGVFIFCWAPFFLHLV 300

Query: 267 FYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPLIYALRSQELRKTFKEIIC 318  
 I+CP NPYC+C+ +HFN YL+LIMCNS+IDPLIYA RS ELR TF+EI+C

Sbjct: 301 LIITCPTNPYCICYTAHFNTYLVLMCNSVIDPLIYAFRSLELRNTFREILC 352

>gi|3024118|sp|P56451|MC5R\_BOVIN MELANOCORTIN-5 RECEPTOR (MC5-R)  
 gi|2511601|emb|CAA05147.1| (AJ002024) melanocortin 5 receptor [Bos taurus]  
 Length = 325

Score = 302 bits (774), Expect = 3e-81  
 Identities = 183/334 (54%), Positives = 222/334 (65%), Gaps = 11/334 (3%)

Query: 1 MNSTHH-HGMHTSLHFWNRSTYGLHSNASEPLGKGYSEGGCYEQLFVSPEVFVTLGVISL 59  
 MNS+ H H + L+ + + GL + L E + ++ EVF+ LG+ISL

Sbjct: 1 MNSSFHLHFLDLGLNTTDGNLSGLSVQNASSL-----CEDMGIAVEVFLALGLISL 51

Query: 60 LENILVIVAIKKNLHSPMYFFICSLAVADMLVSVSNGSETIVITLL-NSTD TDAQSFT 118  
 LENILVI AI +N+NLH+PMYFF+ SLAVADMLVS+SN ETI I LL N A +  
 Sbjct: 52 LENILVIGAIVRNRNLHTPMYFFVGLAVADMLVSLSNSWETITITIIYLLTNKHLVMADASV 111

Query: 119 VNIDNVIDXXXXXXXXXXXXXXXXXXXXDRYFTIFYALQYHNIMTVKRVGIIISCIWAVCT 178  
 ++DNV D DRY TIF AL+Y IMT +R G II IWA C  
 Sbjct: 112 RHLDNVFDSMICISVVASMCSSLAIADVDTIFCALRYQRIMTGRRSGAIIIGGIWAFCA 171

Query: 179 VSGVLFIIYSDDSAVIICLITVFFTMLALMASLYVHMFLMARLHIKRIAVLPGTGTIRQG 238  
 G +FI+Y +S+ V+ICLI +F TML LMASLY HMFL+AR HI+RIA LPG ++RQ  
 Sbjct: 172 SCGTVFIVYYESTYVVICLIAMFLTMLLLMASLYTHMFLARLTHIRRIATLPGHSSVRQR 231

Query: 239 ANMKGAITLTILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIID 298  
 +KGAITL +L+GVF+VCWAPFFLHLI ISCP N YC CFMSHFN+YLILIMCNS+ID  
 Sbjct: 232 TGVKGAITLAMLLGVFIVCWAPFFLHLILMISCPHNLVYCSCFMHFNMYLILIMCNSVID 291

Query: 299 PLIYALRSQELRKTFKEIICCYPLGGLCDLSSRY 332  
 PLIYA RSQE+RKTFKEI+C C SRY  
 Sbjct: 292 PLIYAFRSQEMRKTFKEIVCFQSFRTPCRFPSTY 325

>gi|1170884|sp|P41983|MC5R\_SHEEP MELANOCORTIN-5 RECEPTOR (MC5-R)  
 gi|632118|pir||S43120 melanocyte-stimulating hormone receptor - sheep  
 gi|7447149|pir||I46416 melanocyte-stimulating hormone receptor - sheep  
 gi|467693|emb|CAA83239.1| (Z31369) melanocyte-stimulating hormone receptor [Ovis ar  
 Length = 325

Score = 300 bits (768), Expect = 1e-80  
 Identities = 183/335 (54%), Positives = 223/335 (65%), Gaps = 13/335 (3%)

Query: 1 MNSTHH-HGMHTSLHFWNRSTYGLH-SNASEPLGKGYSEGGCYEQLFVSPEVFTLGVIS 58  
 MNS+ H H + L+ + GL NAS P E + ++ EVF+ LG+IS  
 Sbjct: 1 MNSSFHLHFLDLGLNATEGNLSGLSVRNASSPC-----EDMGIAVEVFLALGLIS 50

Query: 59 LLENILVIVAIKKNLHSPMYFFICSLAVADMLVSVSNGSETIVITLL-NSTD TDAQSF 117  
 LLENILVI AI +N+NLH PMYFF+ SLAVADMLVS+SN ETI I LL N A +  
 Sbjct: 51 LLENILVIGAIVRNRNLHIPMYFFVGLAVADMLVSLSNFWETITITIIYLLTNKHLVMADAS 110

Query: 118 TVNIDNVIDXXXXXXXXXXXXXXXXXXXXDRYFTIFYALQYHNIMTVKRVGIIISCIWAVC 177  
 ++DNV D DRY TIF L+Y IMT +R G II+ IWA C  
 Sbjct: 111 VRHLDNVFDSMICISVVASMCSSLAIADVDTIFCRLRYQRIMTGRRSGAIIAGIWAFC 170

Query: 178 TVSGVLFIIYSDDSAVIICLITVFFTMLALMASLYVHMFLMARLHIKRIAVLPGTGTIRQ 237  
 T G +FI+Y +S+ V++CLI +F TML LMASLY HMFL+AR H++RIA LPG ++RQ  
 Sbjct: 171 TSCGTVFIVYYESTYVVVCLIAMFLTMLLLMASLYTHMFLARLTHVRRIAALPGHSSVRQ 230

Query: 238 GANMKGAITLTILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSII 297  
 +KGAITL +L+GVF++CWAPFFLHLI ISCPQN YC CFMSHFN+YLILIMCNS+I  
 Sbjct: 231 RTGVKGAITLAMLLGVFIICWAPFFLHLILMISCPQNLYCSCFMHFNMYLILIMCNSVI 290

Query: 298 DPLIYALRSQELRKTFKEIICCYPLGGLCDLSSRY 332  
 DPLIYA RSQE+RKTFKEI+C C S Y  
 Sbjct: 291 DPLIYAFRSQEMRKTFKEIVCFQGFRTPCRFPSTY 325

>gi|417279|sp|P32244|MC3R\_RAT MELANOCORTIN-3 RECEPTOR (MC3-R)  
 gi|480295|pir||S36636 melanocortin receptor 3 - rat  
 gi|2144036|pir||A48254 melanocortin-3 receptor - black rat

gi|396552|emb|CAA50005.1| (X70667) melanocortin-3 receptor [Rattus rattus]  
Length = 323

Score = 297 bits (761), Expect = 8e-80  
Identities = 163/299 (54%), Positives = 213/299 (70%), Gaps = 3/299 (1%)

Query: 23 LHSNASEPLGKGYSEGGCYQLFVSPEVFTLGVISLLENILVIVAIKKNLHSPMYFF 82  
L + + P S G EQ+F+ PEVF+ LG++SL+ENILVI+A+ +N NLHSPMYFF  
Sbjct: 17 LSQHPAAPSASNRSGSGFCEQVFIKPEVFLALGIVSLMENILVILAVVRNGNLHSPMYFF 76

Query: 83 ICSLAVADMLVSVSNGSETIVITLLNSTD-TDAQSFTVNIDNVIDXXXXXXXXXXXXXXXXX 141  
+ SL ADMLVS+SN ETI+I ++NS T F ++DN+ D  
Sbjct: 77 LLSLLQADMLVSLSNSLETIMIVVINSDSLTLLEDQFIQHMDNIFDSMICISLVASICNLL 136

Query: 142 XXXXDRTYFTIFYALQYHNIMTVKRVGIIISCIWAVCTVSGVLFIIYSDSSAVIICLITVF 201  
DRY TIFYAL+YH+IMTV++ +I IW C + GV+FI+YS+S VI+CLIT+F  
Sbjct: 137 AIAVDRTYFTIFYALRYHSIMTVRKALSLIVAIWVCCGICGVMFIVYSESKMVIVCLITMF 196

Query: 202 FTMLALMASLYVHMFLMARLHIKRIAVLPGTGTI--RQGANMKGAITLTILIGVFVVCWA 259  
F M+ LM +LY+HMFL ARLH++RIA LP + +Q + MKGA+T+TIL+GVF+ CWA  
Sbjct: 197 FAMVLLMGTLYIHMFLFARLHVQRIALPPADGVAPQQHSCMKGAVTITILLGVFIFCWA 256

Query: 260 PFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPLIYALRSQELRKTFKEIIC 318  
PFFLHL+ I+CP NPYC+C+ +HFN YL+LIMCNS+IDPLIYA RS ELR TFKEI+C  
Sbjct: 257 PFFLHLVLIITCPTNPYCICYTAHFNTYLVLMCNSVIDPLIYAFRSLELRNTFKEILC 315

>gi|13629395|sp|Q9MZV8|MC5R\_PIG MELANOCORTIN-5 RECEPTOR  
gi|9081813|gb|AAF82610.1|AF133793\_1 (AF133793) melanocortin-5 receptor [Sus scrofa]  
Length = 294

Score = 293 bits (749), Expect = 2e-78  
Identities = 170/290 (58%), Positives = 207/290 (70%), Gaps = 4/290 (1%)

Query: 23 LHSNASEPLGKGYSEGGCY---EQLFVSPEVFTLGVISLLENILVIVAIKKNLHSPM 79  
L NA+E G S G E + + EVF+TLG+ISLLENILVI AIA+NKNLH PM  
Sbjct: 4 LQLNATEGNVSGPSVGNTSSPCEDMGIEVEVFTLGLISLLENILVIGAIARNKNLHVPM 63

Query: 80 YFFICSLAVADMLVSVSNGSETIVITLLNSTDTDAQSFTV-NIDNVIDXXXXXXXXXXXXXXXXX 138  
YFF+CSLAVADMLVS+SN ETI I L+ + +V ++DNV D  
Sbjct: 64 YFFVCSLAVADMLVSLNSWETITIIYLIANKHLVLSDTSVRHLDNVFDSDMICISLVASMC 123

Query: 139 XXXXXXXDRYFTIFYALQYHNIMTVKRVGIIISCIWAVCTVSGVLFIIYSDSSAVIICLI 198  
DRY TIFYAL+Y ++MT +R G II+ IWA+CT G +FI+Y +S+ V++CL+  
Sbjct: 124 SLLAVAVDRYVTIFYALRYQHLMGTGRRCGAIAGI WALCTGCGPVFIVYYESTYVVVCLV 183

Query: 199 TVFFTMLALMASLYVHMFLMARLHIKRIAVLPGTGTIRQGANMKGAITLTILIGVFVVCW 258  
+F TML LMASLY HMFL AR H++RIA LPG + RQ +MKGA+TL +L+GVF+VCW  
Sbjct: 184 AMFLTMLLLMASLYAHMFLQARAHVRRIAALPGYRSARQRTSMKGAVTLAMLLGVFIVCW 243

Query: 259 APFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPLIYALRSQE 308  
APFFLHLI ISCPQN YC CFMSHFN+YLILIMCNS+IDPLIYA RSQE  
Sbjct: 244 APFFLHLILMISCPQNLYCSCFMSHFNMYLILIMCNSVIDPLIYAFRSQE 293

>gi|3024117|sp|P56450|MC4R\_MOUSE MELANOCORTIN-4 RECEPTOR (MC4-R)  
gi|2696802|dbj|BAA24015.1| (AB009664) melanocortin 4-receptor [Mus musculus]  
Length = 184

Score = 271 bits (693), Expect = 7e-72  
 Identities = 156/184 (84%), Positives = 162/184 (87%)

Query: 112 TDAQSFTVNIDNVIDXXXXXXXXXXXXXXXXXXXXDRYFTIFYALQYHNIMTVKRVGIIIS 171  
 TDAQSFTVNIDNVID DRYFTIFYALQYHNIMTV+RVGIIIS  
 Sbjct: 1 TDAQSFTVNIDNVIDSVICSSLLASICSLLSIAVDRYFTIFYALQYHNIMTVRRVGIIIS 60

Query: 172 CIWAVCTVSGVLFIIYSDSSAVIICLITVFFTMLALMASLYVHMFLMARLHIKRIAVLPG 231  
 CIWA CTVSGVLFIIYSDSSAVIICLI++FFTML LMASLYVHMFLMARLHIKRIAVLPG  
 Sbjct: 61 CIWAACVTVSGVLFIIYSDSSAVIICLISMFFTMLVLMASLYVHMFLMARLHIKRIAVLPG 120

Query: 232 TGTIRQGANMKGAITLTILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILI 291  
 TGTIRQG NMKGAITLTILIGVFVVCWAPFFLHL+FYISCPQNPYCVCFMSHFNLYLIL+  
 Sbjct: 121 TGTIRQGTNMKGAITLTILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILM 180

Query: 292 MCNS 295  
 MCN+  
 Sbjct: 181 MCNA 184

>gi|7447146|pir||S71420 melanocortin 1 receptor - chicken  
 Length = 314

Score = 256 bits (653), Expect = 2e-67  
 Identities = 147/305 (48%), Positives = 206/305 (67%), Gaps = 7/305 (2%)

Query: 16 WNRSTYGLHSNASEPLGKGYSEGGCYEQLFVSPEVFTLGVISLLENILVIVAIKKNL 75  
 WN S G SNA+ G + +G L + E+F+TLG++SL+EN+LV+ AI KN+NL  
 Sbjct: 14 WNASE-GNQSNTAGAGGAWCQG-----LDIPNELFTLGLVSLVENLLVVAAILKNRNL 67

Query: 76 HSPMYFFICSLAVADMLVSVSNGSETIVITLL-NSTD TDAQSFTVNIDNVIDXXXXXXXXX 134  
 HSPMY+FIC LAV+DMLVSVSN +ET+ + L+ + S ++DNVID  
 Sbjct: 68 HSPMYFICCLAVSDMLVSVSNLAETLFMLLMEHGVLVIRASIVRHMDNVIDMLICSSVV 127

Query: 135 XXXXXXXXXXXXDRYFTIFYALQYHNIMTVKRVGIIISCIWAVCTVSGVLFIIYSDSSAVI 194  
 DRY IFYAL+YH+IMT++R + ++ +W TVS + I Y ++A++  
 Sbjct: 128 SSLSFLGVIAVDYIAIFYALRYHSIMTLQRAVVTMASVWLASTVSSTVLITYYRNAIL 187

Query: 195 ICLITVFFTMLALMASLYVHMFLMARLHIKRIAVLPGTGTIRQGANMKGAITLTILIGVF 254  
 +CLI F ML LM LY+HMF +AR H++ I+ TI + +++KGA+TLTIL+GVF  
 Sbjct: 188 LCLIGFFLFMLVLMVLYIHMFAALARHHVRSISSQQKQPTIYRTSSLKGAVTLTILLGVF 247

Query: 255 VVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPLIYALRSQELRKTFR 314  
 +CW PFF HLI ++CP NP+C CF S+FNL+LILI+CNS++DPLIYA RSQELR+T +  
 Sbjct: 248 FICWGPFFFHLILIVTCPTNPFCCTCFFSYFNLFLILIIICNSVVDPLIYA FRSQELRRTL 307

Query: 315 EIICC 319  
 E++ C  
 Sbjct: 308 EVVLC 312

>gi|13958120|gb|AAK50813.1| (AF362606) melanocortin 1 receptor [Tangara cucullata]  
 Length = 314

Score = 253 bits (647), Expect = 1e-66  
 Identities = 145/304 (47%), Positives = 203/304 (66%), Gaps = 6/304 (1%)

Query: 17 NRSTYGLHSNASEPLGKGYSEGGCYEQLFVSPEVFTLGVISLLENILVIVAIKKNLNH 76  
 + ++ G HSNA+ G G+ +G L + E+F+ LG++SL+EN+LV+ AI KN+NLH  
 Sbjct: 14 SNAEGNHSNATVGAGGGWCQG-----LDIPSELFLALGLVSLVENLLVVAAILKNRNLH 68

Query: 77 SPMYFFICSLAVADMLVSVSNGSETIVITLL-NSTD TDAQSFTVNIDNVIDXXXXXXXXXX 135  
 SP Y+FIC LAV+DMLVS+SN +E + + LL + S ++D+VID  
 Sbjct: 69 SPTYFFICCLAVSDMLVSI SNLAEMLFMLLLEHGVLV MRPSIVRHMDSVIDTLCSSVFS 128

Query: 136 XXXXXXXXXXXXDRYFTIFYALQYHNIMTVKRVGIIISCIWAVCTVSGVLFIIYSDSSAVII 195  
 DRY TIFYAL+YH+IMT++R + ++ +W TVS + I Y S+ V++  
 Sbjct: 129 SLSFLGVIAVDRIYITIFYALRYHSIMTLQRAVVTMASVWLASTVSSTVLIAYYRSNTVLL 188

Query: 196 CLITVFFTMLALMASLYVHMFLMARLHIKRIAVLPGTGTIRQGANMKGAITLTILIGVVFV 255  
 CLI F ML LM LY+HMF +AR H+ I+ T +G ++KGA+TLTIL+GVF  
 Sbjct: 189 CLIGFFLFMLVLMLVLYIHMFA LARHHLHSISSQQKPPTAHRGGLKGA VTLTILLGVVF 248

Query: 256 VCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPLIYALRSQELRKT FKE 315  
 +CW PFF HLI ++CP NP+C CF S+FNL+LILI+CNS+IDPLIYA RSQELR+T +E  
 Sbjct: 249 ICWGPFFFHLILIVTCPTNPFCTCFFSYFNLFLILIICNSVIDPLIYAFRSQELRRTLRE 308

Query: 316 IICC 319  
 ++ C  
 Sbjct: 309 VVTC 312

>gi 13958058 qb AAK50782.1	(AF362575)	melanocortin 1 receptor	[Coereba flaveola]
gi 13958060 qb AAK50783.1	(AF362576)	melanocortin 1 receptor	[Coereba flaveola]
gi 13958062 qb AAK50784.1	(AF362577)	melanocortin 1 receptor	[Coereba flaveola]
gi 13958066 qb AAK50786.1	(AF362579)	melanocortin 1 receptor	[Coereba flaveola]
gi 13958068 qb AAK50787.1	(AF362580)	melanocortin 1 receptor	[Coereba flaveola]
gi 13958070 qb AAK50788.1	(AF362581)	melanocortin 1 receptor	[Coereba flaveola]
gi 13958072 qb AAK50789.1	(AF362582)	melanocortin 1 receptor	[Coereba flaveola]
gi 13958078 qb AAK50792.1	(AF362585)	melanocortin 1 receptor	[Coereba flaveola]
gi 13958082 qb AAK50794.1	(AF362587)	melanocortin 1 receptor	[Coereba flaveola]
gi 13958084 qb AAK50795.1	(AF362588)	melanocortin 1 receptor	[Coereba flaveola]
gi 13958086 qb AAK50796.1	(AF362589)	melanocortin 1 receptor	[Coereba flaveola]
gi 13958088 qb AAK50797.1	(AF362590)	melanocortin 1 receptor	[Coereba flaveola]
gi 13958090 qb AAK50798.1	(AF362591)	melanocortin 1 receptor	[Coereba flaveola]
gi 13958092 qb AAK50799.1	(AF362592)	melanocortin 1 receptor	[Coereba flaveola]
gi 13958094 qb AAK50800.1	(AF362593)	melanocortin 1 receptor	[Coereba flaveola]
gi 13958096 qb AAK50801.1	(AF362594)	melanocortin 1 receptor	[Coereba flaveola]
gi 13958098 qb AAK50802.1	(AF362595)	melanocortin 1 receptor	[Coereba flaveola]
gi 13958100 qb AAK50803.1	(AF362596)	melanocortin 1 receptor	[Coereba flaveola]
gi 13958102 qb AAK50804.1	(AF362597)	melanocortin 1 receptor	[Coereba flaveola]
gi 13958104 qb AAK50805.1	(AF362598)	melanocortin 1 receptor	[Coereba flaveola]
gi 13958106 qb AAK50806.1	(AF362599)	melanocortin 1 receptor	[Coereba flaveola]
gi 13958108 qb AAK50807.1	(AF362600)	melanocortin 1 receptor	[Coereba flaveola]

Length = 314

Score = 253 bits (645), Expect = 2e-66

Identities = 144/304 (47%), Positives = 203/304 (66%), Gaps = 6/304 (1%)

Query: 17 NRSTYGLHSNASEPLGKGYSEGGCYEQLFVSPEVFTLGVISLLENILVIVAIKKNLNH 76  
 + ++ G HSNA+ G G+ +G L + E+F+ LG++SL+EN+LV+ AI KN+NLH  
 Sbjct: 14 SNAEGNHSNATVGAGGGWCQG-----LDIPNELFLALGLVSLVENLLVVAAILKNRNLH 68

Query: 77 SPMYFFICSLAVADMLVSVSNGSETIVITLL-NSTD TDAQSFTVNIDNVIDXXXXXXXXXX 135  
 SP Y+FIC LAV+DMLVS+SN +E + + LL + S ++D+VID  
 Sbjct: 69 SPTYFFICCLAVSDMLVSI SNLAEMLFMLLLEHGVLV MRPSIVRHMDSVIDTLCSSVVS 128

Query: 136 XXXXXXXXXXXXDRYFTIFYALQYHNIMTVKRVGIIISCIWAVCTVSGVLFIIYSDSSAVII 195  
 DRY TIFYAL+YH+IMT++R + ++ +W TVS + I Y S+ +++  
 Sbjct: 129 SLSFLGVIAVDRIYITIFYALRYHSIMTLQRAVVMTASVWLASTVSSTVLIAYYRSNTILL 188

Query: 196 CLITVFFTMLALMASLYVHMFLMARLHIKRIAVLPGTGTIRQGANMKGAITLTILIGVVFV 255  
 CLI F ML LM LY+HMF +AR H+ I+ T +G ++KGA+TLTIL+GVF  
 Sbjct: 189 CLIGFFLFMLVLMLVLYIHMFAALARHHLHSISSQQKPPTAHRGGSCLKGAVTLTILLGVFF 248

Query: 256 VCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPLIYALRSQELRKTFKE 315  
 +CW PFF HLI ++CP NP+C CF S+FNL+LILI+CNS+IDPLIYA RSQELR+T +E  
 Sbjct: 249 ICWGPFFFHLILIVTCPTNPFCACFFSYFNLFLILIIICNSVIDPLIYAFRSQELRRTLRE 308

Query: 316 IICC 319  
 ++ C  
 Sbjct: 309 VVTC 312

>gi|13958064|gb|AAK50785.1| (AF362578) melanocortin 1 receptor [Coereba flaveola]  
gi|13958074|gb|AAK50790.1| (AF362583) melanocortin 1 receptor [Coereba flaveola]  
 Length = 314

Score = 252 bits (644), Expect = 3e-66  
 Identities = 143/304 (47%), Positives = 203/304 (66%), Gaps = 6/304 (1%)

Query: 17 NRSTYGLHSNASEPLGKGYSEGGCYEQLFVSPEVFTLVGLVISLLENILVIVAIKKNLH 76  
 + ++ G HSNA+ G G+ +G L + E+F+ LG++SL+EN+LV+ A+ KN+NLH  
 Sbjct: 14 SNASEGNHSNATVGAGGGWCQG-----LDIPNELFLALGLVSLVENLLVVA AVLKRNRLH 68

Query: 77 SPMYFFICSLAVADMLVSVSNGSETIVITLL-NSTDDAQSFTVNIDNVIDXXXXXXXXXX 135  
 SP Y+FIC LAV+DMLVS+SN +E + + LL + S ++D+VID  
 Sbjct: 69 SPTYFFICCLAVSDMLVSI SNLAEMLFMLLLEHGVLVMRPSIVRHMDSVIDTLICSSVVS 128

Query: 136 XXXXXXXXXXXXDRYFTIFYALQYHNIMTVKRVGIIISCIWAVCTVSGVLFIIYSDSSAVII 195  
 DRY TIFYAL+YH+IMT++R + ++ +W TVS + I Y S+ +++  
 Sbjct: 129 SLSFLGVIAVDRIYITIFYALRYHSIMTLQRAVVMTASVWLASTVSSTVLIAYYRSNTILL 188

Query: 196 CLITVFFTMLALMASLYVHMFLMARLHIKRIAVLPGTGTIRQGANMKGAITLTILIGVVFV 255  
 CLI F ML LM LY+HMF +AR H+ I+ T +G ++KGA+TLTIL+GVF  
 Sbjct: 189 CLIGFFLFMLVLMLVLYIHMFAALARHHLHSISSQQKPPTAHRGGSCLKGAVTLTILLGVFF 248

Query: 256 VCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPLIYALRSQELRKTFKE 315  
 +CW PFF HLI ++CP NP+C CF S+FNL+LILI+CNS+IDPLIYA RSQELR+T +E  
 Sbjct: 249 ICWGPFFFHLILIVTCPTNPFCACFFSYFNLFLILIIICNSVIDPLIYAFRSQELRRTLRE 308

Query: 316 IICC 319  
 ++ C  
 Sbjct: 309 VVTC 312

>gi|13958076|gb|AAK50791.1| (AF362584) melanocortin 1 receptor [Coereba flaveola]  
 Length = 314

Score = 252 bits (643), Expect = 3e-66  
 Identities = 143/304 (47%), Positives = 203/304 (66%), Gaps = 6/304 (1%)

Query: 17 NRSTYGLHSNASEPLGKGYSEGGCYEQLFVSPEVFTLVGLVISLLENILVIVAIKKNLH 76  
 + ++ G HSNA+ G G+ +G L + E+F+ LG++SL+EN+LV+ A+ KN+NLH

Sbjct: 14 SNASEGNHSNATVGAGGGWCQG-----LDIPNELFLALGLVSLVENLLVVA AVLKNRNLH 68

Query: 77 SPMYFFICSLAVADMLVSVSNGSETIVITLL-NSTD TDAQSFTVNIDNVIDXXXXXXXXXX 135  
 SP Y+FIC LAV+DMLVS+SN +E + + LL + S ++D+VID

Sbjct: 69 SPTYFFICCLAVSDMLVSI SNLAEMLFMLLLEHGVLMRPSIVRHMD SVIDTLICSSVVS 128

Query: 136 XXXXXXXXXXXXDRYFTIFYALQYHNIMTVKRVGIIISCIWAVCTVSGVLFIIYSDSSAVII 195  
 DRY TIFYAL+YH+IMT++R + ++ +W TVS + I Y S+ +++

Sbjct: 129 SLSFLGVIAVDRIYITIFYALRYHSIMTLQRAVVMTASVWLASTVSSTVLITYYRSNTILL 188

Query: 196 CLITVFFTMLALMASLYVHMFLMARLHIKRIAVLPGTGTIRQGANMKGAITLTILIGV FV 255  
 CLI F ML LM LY+HMF +AR H+ I+ T +G ++KGA+TLTIL+GVF

Sbjct: 189 CLIGFFLFMLVLMLVLYIHM FALARHHLHSISSQQKPPTAHRGGS LKGA VTLTILLGVFF 248

Query: 256 VCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPLIYALRSQELRKTFKE 315  
 +CW PFF HLI ++CP NP+C CF S+FNL+LILI+CNS+IDPLIYA RSQELR+T +E

Sbjct: 249 ICWGPFFFHLILIVTCPTNPFCACFFSYFNLFLILII CNSVIDPLIYAFRSQELRRTLRE 308

Query: 316 IICC 319  
 ++ C

Sbjct: 309 VVTC 312

>gi|13958110|gb|AAK50808.1| (AF362601) melanocortin 1 receptor [Coereba flaveola]  
gi|13958114|gb|AAK50810.1| (AF362603) melanocortin 1 receptor [Coereba flaveola]  
 Length = 314

Score = 251 bits (641), Expect = 6e-66  
 Identities = 143/304 (47%), Positives = 203/304 (66%), Gaps = 6/304 (1%)

Query: 17 NRSTYGLHSNASEPLGKGYSEGGCYQLFVSPEVFVTLGVISLLENILVIVAIKKNKLNH 76  
 + ++ G HSNA+ G G+ +G L + E+F+ LG++SL+EN+LV+ AI KN+NLH

Sbjct: 14 SNASEGNHSNATVGAGGGWCQG-----LDIPNELFLALGLVSLVENLLVVAAILKNRNLH 68

Query: 77 SPMYFFICSLAVADMLVSVSNGSETIVITLL-NSTD TDAQSFTVNIDNVIDXXXXXXXXXX 135  
 SP Y+FIC LAV+DMLVS+SN ++ + + LL + S ++D+VID

Sbjct: 69 SPTYFFICCLAVSDMLVSI SNLAKMLFMLLLEHGVLMRPSIVRHMD SVIDTLICSSVVS 128

Query: 136 XXXXXXXXXXXXDRYFTIFYALQYHNIMTVKRVGIIISCIWAVCTVSGVLFIIYSDSSAVII 195  
 DRY TIFYAL+YH+IMT++R + ++ +W TVS + I Y S+ +++

Sbjct: 129 SLSFLGVIAVDRIYITIFYALRYHSIMTLQRAVVMTASVWLASTVSSTVLITYYRSNTILL 188

Query: 196 CLITVFFTMLALMASLYVHMFLMARLHIKRIAVLPGTGTIRQGANMKGAITLTILIGV FV 255  
 CLI F ML LM LY+HMF +AR H+ I+ T +G ++KGA+TLTIL+GVF

Sbjct: 189 CLIGFFLFMLVLMLVLYIHM FALARHHLHSISSQQKPPTAHRGGS LKGA VTLTILLGVFF 248

Query: 256 VCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPLIYALRSQELRKTFKE 315  
 +CW PFF HLI ++CP NP+C CF S+FNL+LILI+CNS+IDPLIYA RSQELR+T +E

Sbjct: 249 ICWGPFFFHLILIVTCPTNPFCACFFSYFNLFLILII CNSVIDPLIYAFRSQELRRTLRE 308

Query: 316 IICC 319  
 ++ C

Sbjct: 309 VVTC 312

>gi|13958116|gb|AAK50811.1| (AF362604) melanocortin 1 receptor [Coereba flaveola]  
 Length = 314

Score = 251 bits (640), Expect = 9e-66  
Identities = 143/304 (47%), Positives = 203/304 (66%), Gaps = 6/304 (1%)

Query: 17 NRSTYGLHSNASEPLGKGYSEGGCYEQLFVSPEVFTLGVISLLENILVIVAIKKNLNH 76  
+ ++ G HSNA+ G G+ +G L + E+F+ LG++SL+EN+LV+ AI KN+NLH  
Sbjct: 14 SNASEGNHSNATVGAGGGWCQG-----LDIPNELFLALGLVSLVENLLVVAAILKNRNLH 68

Query: 77 SPMYFFICSLAVADMLVSVSNGSETIVITLL-NSTD TDAQSFTVNIDNVIDXXXXXXXXX 135  
SP Y+FIC LAV+DMLVS+SN ++ + + LL + S ++D+VID  
Sbjct: 69 SPTYFFICCLAVSDMLVSI SNLAKMLFMLLLEHGVLVMRPSIVRHMSVIDTLICSSVVS 128

Query: 136 XXXXXXXXXXXXDRYFTIFYALQYHNIMTVKRVGIIISCIWAVCTVSGVLFIIYSDSSAVII 195  
DRY TIFYAL+YH+IMT++R + ++ +W TVS + I Y S+ +++  
Sbjct: 129 SLSFLGVIAVDRIYITIFYALRYHSIMTLQRAVVTMAIVWLASTVSSTVLITYYRSNTILL 188

Query: 196 CLITVFFTMLALMASLYVHMFLMARLHIKRIAVLPGTGTIRQGANMKGAITLTILIGVVF 255  
CLI F ML LM LY+HMF +AR H+ I+ T +G ++KGA+TLTIL+GVF  
Sbjct: 189 CLIGFFLFMLVLMLVLYIHMFA LARHHLHSISSQKPPPTAHRGGS LKGA VTLTILLGVFF 248

Query: 256 VCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPLIYALRSQELRKTFKE 315  
+CW PFF HLI ++CP NP+C CF S+FNL+LILI+CNS+IDPLIYA RSQELR+T +E  
Sbjct: 249 ICWGPFFFHLILIVTCPTNPFCACFFSYFNLFLILIIICNSVIDPLIYAFRSQELRRTLRE 308

Query: 316 IICC 319  
++ C  
Sbjct: 309 VVTC 312

>gi|13958080|gb|AAK50793.1| (AF362586) melanocortin 1 receptor [Coereba flaveola]  
Length = 314

Score = 250 bits (638), Expect = 1e-65  
Identities = 143/304 (47%), Positives = 202/304 (66%), Gaps = 6/304 (1%)

Query: 17 NRSTYGLHSNASEPLGKGYSEGGCYEQLFVSPEVFTLGVISLLENILVIVAIKKNLNH 76  
+ ++ G HSNA+ G+ +G L + E+F+ LG++SL+EN+LV+ AI KN+NLH  
Sbjct: 14 SNASEGNHSNATVGASGGWCQG-----LDIPNELFLALGLVSLVENLLVVAAILKNRNLH 68

Query: 77 SPMYFFICSLAVADMLVSVSNGSETIVITLL-NSTD TDAQSFTVNIDNVIDXXXXXXXXX 135  
SP Y+FIC LAV+DMLVS+SN +E + + LL + S ++D+VID  
Sbjct: 69 SPTYFFICCLAVSDMLVSI SNLAEMLFMLLLEHGVLVMRPSIVRHMSVIDTLICSSVVS 128

Query: 136 XXXXXXXXXXXXDRYFTIFYALQYHNIMTVKRVGIIISCIWAVCTVSGVLFIIYSDSSAVII 195  
DRY TIFYAL+YH+IMT++R + ++ +W TVS + I Y S+ +++  
Sbjct: 129 SLSFLGVIAVDRIYITIFYALRYHSIMTLQRAVVTMASVWLASTVSSTVLIAYYRSNTILL 188

Query: 196 CLITVFFTMLALMASLYVHMFLMARLHIKRIAVLPGTGTIRQGANMKGAITLTILIGVVF 255  
CLI F ML LM LY+HMF +AR H+ I+ T +G ++KGA+TLTIL+GVF  
Sbjct: 189 CLIGFFLFMLVLMLVLYIHMFA LARHHLHSISSQKPPPTAHRGGS LKGA VTLTILLGVFF 248

Query: 256 VCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPLIYALRSQELRKTFKE 315  
+CW PFF HLI ++CP NP+C CF S+FNL+LILI+CNS+IDPLIYA RSQELR+T +E  
Sbjct: 249 ICWGPFFFHLILIVTCPTNPFCACFFSYFNLFLILIIICNSVIDPLIYAFRSQELRRTLRE 308

Query: 316 IICC 319  
++ C  
Sbjct: 309 VVTC 312



>gi|1709125|sp|P55167|MSHR\_CHICK MELANOCYTE STIMULATING HORMONE RECEPTOR (MSH-R) (ME  
RECEPTOR) (MELANOCORTIN-1 RECEPTOR) (MC1-R)  
gi|1065995|dbj|BAA11336.1| (D78272) melanocortin 1-receptor [Gallus gallus]  
Length = 314

Score = 250 bits (638), Expect = 2e-65  
Identities = 145/305 (47%), Positives = 205/305 (66%), Gaps = 7/305 (2%)

Query: 16 WNRSTYGLHSNASEPLGKGYSEGGCYEQLFVSPEVFTLGVISLLENILVIVAIKKNL 75  
WN S G SNA+ G + +G L + E+F+TLG++SL+EN+LV+ AI KN+NL  
Sbjct: 14 WNASE-GNQSNATAGAGGAWCQG-----LDIPNELFLTGLVSLVENLLVVAAILKNRNL 67

Query: 76 HSPMYFFICSLAVADMLVSVSNGSETIVITLL-NSTD TDAQSFTVNIDNVIDXXXXXXXXX 134  
HSP Y+FIC LAV+DMLVSVSN ++T+ + L+ + S ++DNVID  
Sbjct: 68 HSPTYFFICCLAVSDMLVSVSNLAKTLFMLLMEHGVLVIRASIVRHMDNVIDMLICSSVV 127

Query: 135 XXXXXXXXXXXXDRYFTIFYALQYHNIMTVKRVGIIISCIWAVCTVSGVLFIIYSDSSAVI 194  
DRY TIFYAL+YH+IMT++R + ++ +W TVS + I Y ++A++  
Sbjct: 128 SLSFLGVIAVDYITIFYALRYHSIMTLQRAVVTMASVWLASTVSSTVLITYYRNAIL 187

Query: 195 ICLITVFFTMLALMASLYVHMFMLMARLHIKRIAVLPGTGTIRQGANMKGAITLTILIGVF 254  
+CLI F ML LM LY+HMF +A H++ I+ TI + +++KGA+TLTIL+GVF  
Sbjct: 188 LCLIGFFLFMLVLMVLVLIHMFALACHHVRSSISSQQKQPTIYRTSSLKGAVTLTILLGVF 247

Query: 255 VVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPLIYALRSQELRKTFK 314  
+CW PFF HLI ++CP NP+C CF S+FNL+LILI+CNS++DPLIYA RSQELR+T +  
Sbjct: 248 FICWGPFFFHLILIVTCPTNPFCCTCFSSYFNLFLILICNSVVDPLIYAFRSQELRRTL 307

Query: 315 EIICC 319  
E++ C  
Sbjct: 308 EVVLC 312

>gi|13958112|gb|AAK50809.1| (AF362602) melanocortin 1 receptor [Coereba flaveola]  
gi|13958118|gb|AAK50812.1| (AF362605) melanocortin 1 receptor [Coereba flaveola]  
Length = 314

Score = 249 bits (637), Expect = 2e-65  
Identities = 143/304 (47%), Positives = 202/304 (66%), Gaps = 6/304 (1%)

Query: 17 NRSTYGLHSNASEPLGKGYSEGGCYEQLFVSPEVFTLGVISLLENILVIVAIKKNLH 76  
+ ++ G HSNA+ G G+ +G L + E+F+ LG++SL+EN+LV+ AI KN+NLH  
Sbjct: 14 SNASEGNHSNATVGAGGGWCQG-----LDIPNELFLALGLVSLVENLLVVAAILKNRNLH 68

Query: 77 SPMYFFICSLAVADMLVSVSNGSETIVITLL-NSTD TDAQSFTVNIDNVIDXXXXXXXXX 135  
SP Y+FIC LAV+DMLVS+SN + + + LL + S ++D+VID  
Sbjct: 69 SPTYFFICCLAVSDMLVSVSNLVKMLFMLLLEHGVLVMRPSIVRHMDSVIDTLICSSVVS 128

Query: 136 XXXXXXXXXXXXDRYFTIFYALQYHNIMTVKRVGIIISCIWAVCTVSGVLFIIYSDSSAVII 195  
DRY TIFYAL+YH+IMT++R + ++ +W TVS + I Y S+ +++  
Sbjct: 129 SLSFLGVIAVDYITIFYALRYHSIMTLQRAVVTMASVWLASTVSSTVLITYYRSNTILL 188

Query: 196 CLITVFFTMLALMASLYVHMFMLMARLHIKRIAVLPGTGTIRQGANMKGAITLTILIGVFV 255  
CLI F ML LM LY+HMF +AR H+ I+ T +G ++KGA+TLTIL+GVF  
Sbjct: 189 CLIGFFLFMLVLMVLVLIHMFALARHHLHSISSQQKPPTAHRGGSLSKGAVTLTILLGVFF 248

Query: 256 VCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPLIYALRSQELRKTFKE 315  
+CW PFF HLI ++CP NP+C CF S+FNL+LILI+CNS+IDPLIYA RSQELR+T +E

Sbjct: 249 ICWGPFFFHLILIVTCPTNPFCACFFSYFNLFLILIIICNSVIDPLIYAFRSQELRRTLRE 308

Query: 316 IICC 319

++ C

Sbjct: 309 VVTC 312

>gi|2134364|pir|S70005 melanocortin 1 receptor - chicken

Length = 314

Score = 249 bits (637), Expect = 2e-65

Identities = 145/305 (47%), Positives = 205/305 (66%), Gaps = 7/305 (2%)

Query: 16 WNRSTYGLHSNASEPLGKGYSEGGCYEQLFVSPEVFTLGVISLLENILVIVAIKKNL 75

WN S G SNA+ G + +G L + E+F+TLG++SL+EN+LV+ AI KN+NL

Sbjct: 14 WNASE-GNQSNATAGAGAWCQG-----LDIPNELFLTGLVSLVENLLVVAAILKNRNL 67

Query: 76 HSPMYFFICSLAVADMLVSVSNGSETIVITLL-NSTDDAQSFTVNIDNVIDXXXXXXXXX 134

HSP Y+FIC LAV+DMLVSVSN ++T+ + L+ + S ++DNVID

Sbjct: 68 HSPTYFFICCLAVSDMLVSVSNLAKTLFMLMEHGVLVIRASIVRHMDNVIDMLICSSVV 127

Query: 135 XXXXXXXXXXXXDRYFTIFYALQYHNIMTVKRVGIIISCIWAVCTVSGVLFIIYSDSSAVI 194

DRY TIFYAL+YH+IMT++R + ++ +W TVS + I Y ++A++

Sbjct: 128 SSLSFLGVIAVDRIYITIFYALRYHSIMTLQRAVVTMASVWLASTVSSTVLITYYRNAIL 187

Query: 195 ICLITVFFTMLALMASLYVHMFLMARLHIKRIAVLPGTGTIRQGANMKGAITLTILIGVF 254

+CLI F ML LM LY+HMF +A H++ I+ TI + +++KGA+TLTIL+GVF

Sbjct: 188 LCLIGFFLMLVLMVLYIHMALACHHVRTISSQQKQPTIYRTSSLKGAVTLTILLGVF 247

Query: 255 VVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPLIYALRSQELRKTFK 314

+CW PFF HLI ++CP NP+C CF S+FNL+LILI+CNS++DPLIYA RSQELR+T +

Sbjct: 248 FICWGPFFFHLILIVTCPTNPFCCTCFSSYFNLFLILIIICNSVVDPLIYAFRSQELRRTL 307

Query: 315 EIICC 319

E++ C

Sbjct: 308 EVVLC 312

>gi|6091553|gb|AAC48590.2| (U39469) alpha melanocyte stimulating hormone receptor [B

Length = 317

Score = 249 bits (635), Expect = 3e-65

Identities = 138/272 (50%), Positives = 184/272 (66%), Gaps = 2/272 (0%)

Query: 50 VFVTLGVISLLENILVIVAIKKNLHSPMYFFICSLAVADMLVSVSNGSETIVITLLNS 109

+F++LG++SL+EN+LV+ AIAKN+NLHSPMY+FIC LAV+D+LVSVSN ET V+ LL +

Sbjct: 44 LFLSLGLVSLVENVLVVAIAKKNRNLHSPMYFFICCLAVSDLLVSVSNVLETAVMPLLEA 103

Query: 110 TDTDAQSFTV-NIDNVIDXXXXXXXXXXXXXXXXXXXXRYFTIFYALQYHNIMTVKRVGI 168

Q+ V +DNVID

DRY +IFYAL+YH+++T+ R

Sbjct: 104 GVLATQAAVVQQLDNVIDVLICGSMVSSLCFLGAIADVDRYISIFYALRYHVVTLPRWR 163

Query: 169 IISCIWAVCTVSGVLFIIYSDSSAVIICLITVFFTMLALMASLYVHMFLMARLHIKRIAV 228

II+ IW ++ +LFI Y + +++CL+ +F MLALMA LYVHM A H + IA

Sbjct: 164 IIAAIWVASILTSLLFITYYNHKVILLCLVGLFIAMALMAVLYVHMLARACQHARGIAR 223

Query: 229 LPGTG-TIRQGANMKGAITLTILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNL 287

L I QG +KGA TLTIL+GVF +CW PFFLHL + CPQ+P C C +FNL+

Sbjct: 224 LQKRQRPIHQGFGLKGAATLTILLGVFFLCWGPFFLHLSLIVLCPQHPTCGCIFKNFNLF 283

Query: 288 LILIMCNSIIDPLIYALRSQELRKTFKEIICC 319  
L LI+CN+I+DPLIYA RSQELRKT +E++ C

Sbjct: 284 LALIICNAIVDPLIYAFRSQELRKTLQEVLQC 315

>gi|631554|pir||S45708 MSH receptor - bovine  
gi|547326|gb|AAB31361.1| (S71017) melanocortin receptor; BDF3 [Bos taurus]  
Length = 317

Score = 248 bits (634), Expect = 4e-65  
Identities = 138/272 (50%), Positives = 184/272 (66%), Gaps = 2/272 (0%)

Query: 50 VFVTLGVISLLENILVIVAIKKNLHSPMYFFICSLAVADMLVSVSNGSETIVITLLNS 109  
+F++LG++SL+EN+LV+ AIAKN+NLHSPMY+FIC LAV+D+LVSVSN ET V+ LL +  
Sbjct: 44 LFLSLGLVSLVENVLVVAIAKNNLHSPMYFFICCLAVSDLLVSVSNVLETAVMPLLEA 103

Query: 110 TDTDAQSFTV-NIDNVIDXXXXXXXXXXXXXXXXXXXXRYFTIFYALQYHNIMTVKRVGI 168  
Q+ V +DNVID DRY +IFYAL+YH+++T+ R  
Sbjct: 104 GVLATQAAVVQQLDNVIDVLICGSMVSSLCFLGAIADVDRYISIFYALRYHSVVTLPRWR 163

Query: 169 IISCIWAVCTVSGVLFIIYSDSSAVIICLITVFFTMLALMASLYVHMLMARLHIKRIAV 228  
II+ IW ++ +LFI Y + +++CL+ +F MLALMA LYVHM A H + IA  
Sbjct: 164 IIAAIWVASILTSLLFITYYNHKVILLCLVGLFIAMALMAVLYVHMLARACQHARGIAR 223

Query: 229 LPGTG-TIRQGANMKGAITLTILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNL 287  
L I QG +KGA TLTIL+GVF +CW PFFLHL + CPQ+P C C +FNL+  
Sbjct: 224 LQKRQRPIHQGFGLKGAATLTILLGVFFLCWGPFFLHLSLIVLCPQHPTCGCIFKNFNLF 283

Query: 288 LILIMCNSIIDPLIYALRSQELRKTFKEIICC 319  
L LI+CN+I+DPLIYA RSQELRKT +E++ C  
Sbjct: 284 LALIICNAIVDPLIYAFRSQELRKTLQEVLQC 315

>gi|2851404|sp|P47798|MSHR\_BOVIN MELANOCYTE STIMULATING HORMONE RECEPTOR (MSH-R) (ME  
RECEPTOR) (MELANOCORTIN-1 RECEPTOR) (MC1-R) (BDF3)  
gi|2462977|emb|CAA74291.1| (Y13957) melanocyte stimulating hormone receptor [Ovibos  
gi|6687071|emb|CAB64818.1| (Y19103) melanocortin 1-receptor [Bos taurus]  
Length = 317

Score = 248 bits (634), Expect = 4e-65  
Identities = 138/272 (50%), Positives = 184/272 (66%), Gaps = 2/272 (0%)

Query: 50 VFVTLGVISLLENILVIVAIKKNLHSPMYFFICSLAVADMLVSVSNGSETIVITLLNS 109  
+F++LG++SL+EN+LV+ AIAKN+NLHSPMY+FIC LAV+D+LVSVSN ET V+ LL +  
Sbjct: 44 LFLSLGLVSLVENVLVVAIAKNNLHSPMYFFICCLAVSDLLVSVSNVLETAVMLLLEA 103

Query: 110 TDTDAQSFTV-NIDNVIDXXXXXXXXXXXXXXXXXXXXRYFTIFYALQYHNIMTVKRVGI 168  
Q+ V +DNVID DRY +IFYAL+YH+++T+ R  
Sbjct: 104 GVLATQAAVVQQLDNVIDVLICGSMVSSLCFLGAIADVDRYISIFYALRYHSVVTLPRWR 163

Query: 169 IISCIWAVCTVSGVLFIIYSDSSAVIICLITVFFTMLALMASLYVHMLMARLHIKRIAV 228  
II+ IW ++ +LFI Y + +++CL+ +F MLALMA LYVHM A H + IA  
Sbjct: 164 IIAAIWVASILTSLLFITYYNHKVILLCLVGLFIAMALMAVLYVHMLARACQHARGIAR 223

Query: 229 LPGTG-TIRQGANMKGAITLTILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNL 287  
L I QG +KGA TLTIL+GVF +CW PFFLHL + CPQ+P C C +FNL+

Sbjct: 224 LQKRQRPIHQGFGLKGAATLTILLGVFFLCWGPFFLHLSLIVLCPQHPTCGCIFKNFNLF 283

Query: 288 LILIMCNSIIDPLIYALRSQELRKTFKEIICC 319  
L LI+CN+I+DPLIYA RSQELRKT +E++ C

Sbjct: 284 LALIICNAIVDPLIYAFRSQELRKTLQEVLQC 315

>gi|3024181|sp|P56447|MSHR\_OVIMO MELANOCYTE STIMULATING HORMONE RECEPTOR (MSH-R) (ME  
RECEPTOR) (MELANOCORTIN-1 RECEPTOR) (MC1-R)  
gi|2463326|emb|CAA74290.1| (Y13956) melanocyte stimulating hormone receptor [Ovibos  
Length = 317

Score = 244 bits (623), Expect = 7e-64

Identities = 137/272 (50%), Positives = 183/272 (66%), Gaps = 2/272 (0%)

Query: 50 VFVTLGVISLLENILVIVAIKKNLHSPMYFFICSLAVADMLVSVSNGSETIVITLLNS 109  
+F++LG++SL+EN+LV+ AIAKN+NLHSPMY+F+C LA++D+LVSVSN ET V+ LL +

Sbjct: 44 LFLSLGLVSLVENVLVVAIAKKNLHSPMYFVCCCLAMSDLLVSVSNVLETAVMLLLEA 103

Query: 110 TDTDAQSFTV-NIDNVIDXXXXXXXXXXXXXXXXXXXXRYFTIFYALQYHNIMTVKRVGI 168  
Q+ V +DNVID DRY +IFYAL+YH+++T+ R

Sbjct: 104 GVLATQAAVVQQLDNVIDVLICSSMVSSLCFLGAIADVDRYISIFYALRYHSVVTLPRAWR 163

Query: 169 IISCIWAVCTVSGVLFIIYSDSSAVIICLITVFFTMLALMASLYVHMLMARLHIKRIAV 228  
II+ IW ++ VL I Y + + V++CL+ F MLALMA LYVHM A H + IA

Sbjct: 164 IIAAIWVASILTSVLSITYYNHTVLLCLVGGFFIAMLALMAVLYVHMLARACRHARGIAR 223

Query: 229 LPGTG-TIRQGANMKGAITLTILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNL 287  
L I QG +KGA TLTIL+GVF +CW PFFLHL + CPQ+P C C +FNL+

Sbjct: 224 LQKRQRPIHQGFGLKGAATLTILLGVFFLCWGPFFLHLSLIVLCPQHPTCGCIFKNFNLF 283

Query: 288 LILIMCNSIIDPLIYALRSQELRKTFKEIICC 319  
L LI+CN+I+DPLIYA RSQELRKT +E++ C

Sbjct: 284 LALIICNAIVDPLIYAFRSQELRKTLQEVLQC 315

>gi|3024178|sp|P56444|MSHR\_CAPHI MELANOCYTE STIMULATING HORMONE RECEPTOR (MSH-R) (ME  
RECEPTOR) (MELANOCORTIN-1 RECEPTOR) (MC1-R)  
gi|2462994|emb|CAA74292.1| (Y13958) melanocyte stimulating hormone receptor [Ovibos  
Length = 317

Score = 243 bits (621), Expect = 1e-63

Identities = 137/272 (50%), Positives = 183/272 (66%), Gaps = 2/272 (0%)

Query: 50 VFVTLGVISLLENILVIVAIKKNLHSPMYFFICSLAVADMLVSVSNGSETIVITLLNS 109  
+F++LG++SL+EN+LV+ AIAKN+NLHSPMY+FIC LA++D+LVSVSN ET V+ LL +

Sbjct: 44 LFLSLGLVSLVENVLVVAIAKKNLHSPMYFICCLAMSDLLVSVSNVLETAVMLLLEA 103

Query: 110 TDTDAQSFTV-NIDNVIDXXXXXXXXXXXXXXXXXXXXRYFTIFYALQYHNIMTVKRVGI 168  
++ V +DNVID DRY +IFYAL+YH+++T+ R

Sbjct: 104 GVLATRAAAVVQQLDNVIDVLICSSMVSSLCFLGAIADVDRYISIFYALRYHSVVTLPRAWR 163

Query: 169 IISCIWAVCTVSGVLFIIYSDSSAVIICLITVFFTMLALMASLYVHMLMARLHIKRIAV 228  
II+ IW ++ VL I Y + + V++CL+ F MLALMA LYVHM A H + IA

Sbjct: 164 IIAAIWVASILTSVLSITYYNHTVLLCLVGGFFIAMLALMAVLYVHMLARACQHARGIAR 223

Query: 229 LPGTG-TIRQGANMKGAITLTILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNL 287  
L I QG +KGA TLTIL+GVF +CW PFFLHL + CPQ+P C C +FNL+

Sbjct: 224 LQKRQRPIHQGFGLKGAATLTILLGVFFLCWGPFFLHLSLIVLCPQHPTCGCIFKNFNLF 283

Query: 288 LILIMCNSIIDPLIYALRSQELRKTFKEIICC 319  
L LI+CN+I+DPLIYA RSQELRKT +E++ C

Sbjct: 284 LALIICNAIVDPLIYAFRSQELRKTLQEVLQC 315

>gi|3024173|sp|O19037|MSHR\_SHEEP MELANOCYTE STIMULATING HORMONE RECEPTOR (MSH-R) (ME  
RECEPTOR) (MELANOCORTIN-1 RECEPTOR) (MC1-R)  
gi|2463321|emb|CAA74298.1| (Y13965) MC1-R protein [Ovis aries]  
Length = 317

Score = 243 bits (620), Expect = 2e-63

Identities = 137/272 (50%), Positives = 183/272 (66%), Gaps = 2/272 (0%)

Query: 50 VFVTLGVISLLENILVIVAIKKNLHSPMYFFICSLAVADMLVSVSNGSETIVITLLNS 109  
+F++LG++SL+EN+LV+ AIAKN+NLHSPMY+FIC LA++D+LVSVSN ET V+ LL +

Sbjct: 44 LFLSLGLVSLVENVLVVAIAKKNRNLHSPMYFFICCLAMSDDLVSNSVLETAVMLLLEA 103

Query: 110 TDTDAQSFTV-NIDNVIDXXXXXXXXXXXXXXXXXXXXRYFTIFYALQYHNIMTVKRVGI 168  
++ V +DNVID DRY +IFYAL+YH+++T+ R

Sbjct: 104 GVLATRAAVVQQLDNVIDVLICSSMVSSLCFLGAIADVDRYISIFYALRYHSVVTLPRAWR 163

Query: 169 IISCIWAVCTVSGVLFIIYSDSSAVIICLITVFFTMLALMASLYVHMLMARLHIKRIAV 228  
II+ IW ++ VL I Y + + V++CL+ F MLALMA LYVHM A H + IA

Sbjct: 164 IIAAIWVASILTSVLSITYYNHTVVLLCLVGFFIAMLALMAVLYVHMLARACQHARGIAR 223

Query: 229 LPGTG-TIRQGANMKGAITLTILIGVFFVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNL 287  
L I QG +KGA TLTIL+GVF +CW PFFLHL + CPQ+P C C +FNL+

Sbjct: 224 LQKRQRPIHQGFGLKGAATLTILLGVFFLCWGPFFLHLSLIVLCPQHPTCGCIFKNFNLF 283

Query: 288 LILIMCNSIIDPLIYALRSQELRKTFKEIICC 319

L LI+CN+I+DPLIYA RSQELRKT +E++ C

Sbjct: 284 LALIICNAIVDPLIYAFRSQELRKTLQEVLQC 315

>gi|3024177|sp|P56443|MSHR\_CAPCA MELANOCYTE STIMULATING HORMONE RECEPTOR (MSH-R) (ME  
RECEPTOR) (MELANOCORTIN-1 RECEPTOR) (MC1-R)  
gi|2462988|emb|CAA74294.1| (Y13960) melanocyte stimulating hormone receptor [Ovibos  
Length = 317

Score = 242 bits (617), Expect = 4e-63

Identities = 139/272 (51%), Positives = 185/272 (67%), Gaps = 2/272 (0%)

Query: 50 VFVTLGVISLLENILVIVAIKKNLHSPMYFFICSLAVADMLVSVSNGSETIVITLLNS 109  
+F++LG++SL+EN+LV+ AIAKN+NLHSPMY+FIC LAV+D+LVSVSN ET V+ LL +

Sbjct: 44 LFLSLGLVSLVENVLVVAIAKKNRNLHSPMYFFICCLAVSDDLVSNSVLETAVMLLLEA 103

Query: 110 TDTDAQSFTV-NIDNVIDXXXXXXXXXXXXXXXXXXXXRYFTIFYALQYHNIMTVKRVGI 168  
A++ V +DNVID DRY +IFYAL+YH+++T+ R

Sbjct: 104 GALAARAADVQQLDNVIDMLICGSMVSSLCFLGAIADVDRYISIFYALRYHSVVTLPRAWR 163

Query: 169 IISCIWAVCTVSGVLFIIYSDSSAVIICLITVFFTMLALMASLYVHMLMARLHIKRIAV 228  
II+ IW ++ +LFI Y + + V++CL+ F MLALMA LYVHM A H + IA

Sbjct: 164 IIAAIWVASILTSLLFITYYNHTVVLLCLVGFFIAMLALMAVLYVHMLARACQHARGIAR 223

Query: 229 LPGTG-TIRQGANMKGAITLTILIGVFFVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNL 287  
L I QG +KGA TLTIL+GVF +CW PFFLHL + CPQ+P C C +FNL+

Sbjct: 224 LQKRQRPIHQGFGLKGAATLTILLGVFFLCWGPFFLHLSLIVLCPQHPTCGCIFKNFNLF 283

Query: 288 LILIMCNSIIDPLIYALRSQELRKTFKEIICC 319  
L LI+CN+I+DPLIYA RSQELRKT +E++ C

Sbjct: 284 LALIICNAIVDPLIYAFRSQELRKTLQEVLC 315

>gi|14599450|gb|AAK70924.1|AF288357\_1 (AF288357) melanocortin 1 receptor [Equus caba  
Length = 317

Score = 241 bits (616), Expect = 5e-63

Identities = 145/300 (48%), Positives = 191/300 (63%), Gaps = 11/300 (3%)

Query: 22 GLHSNASEPLGKGYSEGCGYEQLFVSPEVFVTLGVISLLENILVIVAIKKNLHSPMYF 81  
GL +N +EP C E + + +F++LG++SL+EN+LV+ AIAKN+NLHSPMY+

Sbjct: 25 GLTTNQTEP-----PCLE-VSIPDGLFSLGLVSLVENVLVVTAIAKNRNLHSPMY 75

Query: 82 FICSLAVADMLVSVSNGSETIVITLLNSTDTAQ-SFTVNIDNVIDXXXXXXXXXXXXXXXXX 140  
FIC LAV+D+LVS+SN E ++ LL + Q S +DN+ID

Sbjct: 76 FICCLAVSDLLVSMNSVLEMAILLLLEAGVLATQASVLQQLDNIIDVLICGSMVSSLCFL 135

Query: 141 XXXXXDRYFTIFYALQYHNIMTVKRVGIIISCIWAVCTVSGVLFIIYSDSSAVIICLITV 200  
DRY +IFYAL+YH+IM + RV I IW V +S LFI Y + +AV++CL+T

Sbjct: 136 GSIAVDRIYISIFYALRYHSIMMLPRVWRAIVAIWVSVLSSTLFIAYYNHTAVLLCLVTF 195

Query: 201 FFTMLALMASLYVHMFMLMARLHIKRIAVL-PGTGTIRQGANMKGAITLTILIGVFFVVCWA 259  
F ML LMA LYVHM A H + IA L I QG +KGA TLTIL+GVF +CW

Sbjct: 196 FVAMLVLMVAVLYVHMLARACQHARGIARLHKRQHPHQGFGLKGAATLTILLGVFFLCWG 255

Query: 260 PFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPLIYALRSQELRKTFKEIICC 319  
PFFLHL I CPQ+P C C +F L+L LI+C++I+DPLIYA RSQELRKT +E++ C

Sbjct: 256 PFFLHLSLLILCPQHPTCGCVFKNFKLFLTLILCSAIVDPLIYAFRSQELRKTLQEVLLC 315

>gi|14276855|gb|AAK58422.1|AF326520\_1 (AF326520) melanocortin 1 receptor [Sus scrofa  
Length = 320

Score = 241 bits (615), Expect = 7e-63

Identities = 137/272 (50%), Positives = 183/272 (66%), Gaps = 2/272 (0%)

Query: 50 VFVTLGVISLLENILVIVAIKKNLHSPMYFFICSLAVADMLVSVSNGSET-IVITLLN 108  
+F++LG++SL+EN+LV+ AIAKN+NLHSPMY+F+C LAV+D+LVS+SN ET +++ L

Sbjct: 47 LFLSLGLVSLVENVLVVAIAKNRNLHSPMYFVCCCLAVSDLLVSVSNVLETAVLLLEA 106

Query: 109 STDTAQSFVTNIDNVIDXXXXXXXXXXXXXXXXXXDRYFTIFYALQYHNIMTVKRVG 168  
+ +DNV+D DRY +IFYAL+YH+I+T+ R G

Sbjct: 107 GALAAQAQAVVQQLDNVMDVLICGSMVSSLCFLGAIADVDRYVSIFYALRYHSIVTLPRAGR 166

Query: 169 IISCIWAVCTVSGVLFIIYSDSSAVIICLITVFFTMLALMASLYVHMFMLMARLHIKRIAV 228  
I+ IWA +S LFI Y +AV++ L++ F MLALMA LYVHM A H + IA

Sbjct: 167 AIAAIWAGSVLSSTLFIAYYHHTAVLLGLVSFFVAMLALMAVLYVHMLARACQHRHIAR 226

Query: 229 LPGTG-TIRQGANMKGAITLTILIGVFFVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLY 287  
L T RQG +KGA TLTIL+GVF++CWAPFFLHL + CPQ+P C C + NL+

Sbjct: 227 LHKTQHPTRQGCGLKGAATLTILLGVFFLCWAPFFLHLSLVVLCVCPQHPTCGCVFKNVNL 286

Query: 288 LILIMCNSIIDPLIYALRSQELRKTFKEIICC 319  
L L++CNSI+DPLIYA RSQELRKT +E++ C

Sbjct: 287 LALVICNSIVDPLIYAFRSQELRKTQLQEVLC 318

>gi|3024176|sp|P56442|MSHR\_ALCAA MELANOCYTE STIMULATING HORMONE RECEPTOR (MSH-R) (ME  
RECEPTOR) (MELANOCORTIN-1 RECEPTOR) (MC1-R)  
gi|2462878|emb|CAA74295.1| (Y13961) melanocyte stimulating hormone receptor [Ovibos  
Length = 317

Score = 241 bits (614), Expect = 9e-63

Identities = 139/272 (51%), Positives = 185/272 (67%), Gaps = 2/272 (0%)

Query: 50 VFVTLGVISLLENILVIVAIKKNLHSPMYFFICSLAVADMLVSVSNGSETIVITLLNS 109  
+F++LG++SL+EN+LV+ AIAKN+NLHSPMY+FIC LAV+D+LVSVSN ET V+ LL +

Sbjct: 44 LFLSLGLVSLVENVLVVAIAKRNRLHSPMYFICCLAVSDLLVSVSNVLETAVMLLLEA 103

Query: 110 TDTDAQSFTV-NIDNVIDXXXXXXXXXXXXXXXXXXXXRYFTIFYALQYHNIMTVKRVGI 168  
A++ V +DNVID DRY +IFYAL+YH+++T+ R

Sbjct: 104 GALAARAAVVQQLDNVIDVLICGSMVSSLCFLGAIAMDRYISIFYALRYHSVVTLPRAWR 163

Query: 169 IISCIWAVCTVSGVLFIIYSDSSAVIICLITVFFTMLALMASLYVHMFMLMARLHIKRIAV 228  
II+ IW ++ +LFI Y + + V++CL+ F MLALMA LYVHM A H + IA

Sbjct: 164 IIAAIWVASILTSLLFITYYNHTVVLLCLVGFFIAMLALMAILYVHMLARACQHARDIAR 223

Query: 229 LPG-TGTIRQGANMKGAITLTILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNL 287  
L I QG +KGA TLTL+GVF +CW PFFLHL + CPQ+P C C +FNL+

Sbjct: 224 LQKRQHPHQGFGLKGAATLTILLGVFFLCWGPFFLHLSLIVLCPQHPTCGCIFKNFNLF 283

Query: 288 LILIMCNSIIDPLIYALRSQELRKTKEIICC 319

L LI+CN+I+DPLIYA RSQELRKT +E++ C

Sbjct: 284 LALIICNAIVDPLIYAFRSQELRKTQLQEVLC 315

Database: nr

Posted date: Sep 17, 2001 12:30 AM

Number of letters in database: 242,018,981

Number of sequences in database: 760,566

Lambda	K	H
0.331	0.142	0.445

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 142,016,099

Number of Sequences: 760566

Number of extensions: 5412194

Number of successful extensions: 24071

Number of sequences better than 10.0: 2377

Number of HSP's better than 10.0 without gapping: 1493

Number of HSP's successfully gapped in prelim test: 886

Number of HSP's that attempted gapping in prelim test: 18501

Number of HSP's gapped (non-prelim): 4307

length of query: 332

length of database: 242,018,981  
effective HSP length: 119  
effective length of query: 213  
effective length of database: 151,511,627  
effective search space: 32271976551  
effective search space used: 32271976551  
T: 11  
A: 40  
X1: 15 ( 7.2 bits)  
X2: 38 (14.6 bits)  
X3: 64 (24.7 bits)  
S1: 40 (21.9 bits)  
S2: 71 (32.0 bits)